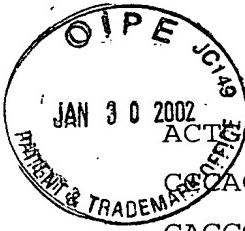


#4

FIGURE 1



ACTGCACCTCGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
 CGACCGTCCGGGCCGGAGCACGGCCGAGGACCTGGAGCTCCGCTGCGTCTCCG
 CAGCGCTACCGCCATGCGCTGCCGCCGGCGCTGGGCTCTGCCCTTGCTG
 CTGCTGCCGCCGCCGGAGGCCAAGAACGCCACGCCCTGCCACCGTGCCGGGCT
 GGTGGACAAGTTAACCAAGGGATGGTGGACACCACAAAGAACAGACTTGGCGGGAAACA
 CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGGAGATC
 CTGGAGGGCTGTGCAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT
 GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGAACCTACGGTCCGACTGTCTCGCATGC
 CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGGAGCAGACA
 GGGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
 ACGGCTACTTCAGCTCGCTCCGAAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
 TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGTGCT
 GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCAGCCCTCCCTGCAGCGCTG
 CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCAAGAGTGTGACTCCAGCTGTG
 GGCTGCACAGGGAAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
 CGGACAGTGTGAGATGTGGACGAGTGCCTACTAGCAGAAAAACCTGTGAGGAAAAACG
 AAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGCTGACGGCTTCGAAGAACG
 GAAGATGCCTGTGCCCCGGCAGAGGCTGAAGCCACAGAACAGGAGAAAGCCGACACAGCT
 GCCCTCCCGGAAGACTAAGTGCCGGACTTACCTTAAATTATTGAGGATGTCC
 CGTGGAAAATGTGGCCCTGAGGATGCCGCTCCTGCAGTGGACAGCGGGAGAGGCTGC
 CTGCTCTCTAACGGTTGATTCTCATTGTCCTTAAACAGCTGCATTCTTGGTTGTTCTTA
 AACAGACTGTATTTGATACAGTTCTTGTAAATAAAATTGACCATTGAGGTAATCAGG
 AGGAAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAACG
 TTGGCCGCCATGGCCAACCTGTTATGGCAGCTATAATGGTTACAAATAAGCAATAGCA
 TCACAAATTTCACAAATAAGCATTTCACTGCATTCTAGTTGGTTGTCACAAACTC
 ATCAATGTATCTTATCATGTCTGGATCGGAATTAATTGGCGCAGCACCATGGCTGAAAT
 AACCTCTGAAAGAGGAACCTGGTAGGTACCTCTGAGGCGAAAGAACCCAGCTGTGGAATG
 TGTGTCAGTTAGGGTGTGAAAGTCCCCAGGCTCCAGCAGGCAGAAGTATGCAAGCATGC
 ATCTCAATTAGTCAGCAACCCAGTTT

2011-07-04 09:54:39

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pi: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAAKKPTPCRCGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIR
LLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCCLACQGGSQRPC
SGNGHCSDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESCKTCSGLTNRDCGECEVGWV
LDEGACVDVDECAAEP PCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SL
AEKTCVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299,
339-343 and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258
and 313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TGCACCTCGGTTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCC CTC
GACCTCGACCCAC CGCGTCCGCCAGGCCAGGGCAGCGGCCAGCGTCAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCATGGCCCGAGGAGCGCCTT
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCTGTGCCTGACTGCCACTGCCGGAGGC
CGGGCCGCCGCAGGAGGAGGCCTGTACCTATGGATCGATGCTCACCAAGGCAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTCAAGAGGGAAAATGGCACCTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTAC
CTGGCAAGCTGCAGGGCAGGCAGAAATACTTCTATGAATTCTGTCCCTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGCCCTCTGCTGGAAACAGTGCCCTCACAGGCA
TCAGTTGTTCAAGTTGGTTCCATGTCTGGAAAACAGGATGGGTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCCAACACCTCAAAATGCTATCT
TCTTTAAAACATGTCAACAAGCTGAGTCCCCAGGCCAGGGTGGCAAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCAGGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCCACGATGTATGAATGGTGGACTTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACGTGACAAAGCAAACGTCAACCAACCTGCTTAAATGGAGGGACC
TGTTTCTACCCCTGGAAAATGTATTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAACCCTGTCGAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGT TACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCAGCCTGGCTGGTCACAT
GGAACCTGCCATGAACCCAAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC
ACACGCCCTCACTAAAAAGGCCGAGGAGCAGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTCATAGCCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCATTAACACTTAAGAATACTGGCCTGAATTATTAGCT
TCATTATAAAATCACTGAGCTGATATTACTCTCCTTTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTGTTCACTGTTAGTACAGCATTCAAGATTTATTGTCAGATATTAGAT
TCAGGTTAAAATTTCAGTGTAGTTGGCAGATATTCAAAATTACAATGCATTATGGT
GTCTGGGGCAGGGAACATCAGAAAGTTAAATTGGGAAAATGCGTAAGTCACAAGAAT
TTGGATGGTCAGTTAATGTTGAAGTTACAGCATTCAAGATTTATTGTCAGATATTAGAT
GTTTGTACATTAAAATTGCTCTAATTAAACTCTCAATACAATATATTGACC
TTACCAATTCCAGAGATTCACTGATTAAAAAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATTCTAAACACAATGAAATAGGAAATATAATGTATGAACTTTGCAT
TGGCTTGAAGCAATATAATATTGTAACAAAACACAGCTTACCTAATAAACATT
ACTGTTGTATGTATAAAATAAGGTGCTGTTAGTTTTGGAAAAAAA
AAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGTCGACCTGCAGAAGCTGGC
CGCCATGGCCAAC TTGTTATTGCAGCTATAATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
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MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVP
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICCPPGLEGEQCEISKCPQPCRNGGKCIKGSKCKCSKGYQGDLCSPKVC
EPGCGAHTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGGTGGCGTCCGGCGTCAGAGCCAGGAGGCAGGCGCAGGCCAGCCTGGG
CCCCAGCCCACACCTTCAACCAGGGCCAGGAGCCACCATTGGCGATGTCCACTGGGCTAC
TGCTGTTGCTGCCGCTGGCACTTGGCTCTGGTGCCAGCAGGGCTGTGGGCCGG
GAGCTAGCACCGGGCTGCACCTGCAGGGCATCCGGACGCCAGGCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCCGCCGTGCCAGCAGACTGTGCCCTGCCACCTGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCAGTGTGCCCTGACTTCTGGACTTC
TGCCTCGGCGTGCACCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGCTGTATCTA
TCCAGTCTTGGGAACGTACTGGACAACGTAAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGCAACTATGGCTGGCAGGCTGG
GAACACAGCGCCTCTGGGCATGACCTGGA**TG**AGGGCATTGCTACCGCCTGGCACCA
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATACAGTGCTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAAGTGGCCAACCTGATTGAGCCTTGA
CCAAGGCAACTGTGAGGCTCTGGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGACACATGACGCCCTGTCCTGCGCCAGAACCTGCTGTCTGTGAC
ACCCACCAGCAGCAGGGCTGCCCGGTGGCGTCTCGATGGTGCCTGGTGGTCTCGTGTG
CCGAGGGTGGTGTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCAGGCATGGTCGGGCAAGCGCCAGGCCACTGCC
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAAATGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCACTCCTGGGCC
CAGCCTGGGCGAGAGGGCCACTTCCGATCGTGCAGGGCTCAATGAGTGCACATCGAG
AGCTTCTGTGCTGGCGCTGGGGCGTGGGATGGAGGACATGGTCATCACTGAGGCTG
CGGGCACACGCCGGTCCGGCTGGGATCCAGGCTAAAGGCCGGCGGAAGAGGCCCAATG
GGCGGTGACCCAGCCTCGCCGACAGAGCCGGGCGCAGGCCGGCGCAAGGCCGCTTAAT
CCCAGGCGGGTCCGCTGACGCAGGCCCGCTGGGAGGCCGGCAGGGAGACTGGCG
GAGCCCCAGACCTCCAGTGGGACGGGAGGGCCTGGGCTGGGAGAGGACACAGCTGCAG
ATCCCAGGCTCTGGGCCACTCAAGACTACCAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCAAATCCCATTCTTTTTTTAGACAGGGCTTGCTCCG
TTGCCAGGTTGGAGTGAGTGCAGTGGCCATCAGGCTCACTGTAACCTCCACTCCTGGTTCA
AGTGACCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACCTGGC
TAATTTTGATTTTGAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCGAACT
CCTGGGCTCAAGCGGTCCACCTGCCCTCCAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTCAAGATATTATTTCTTCACTGTTAAAA
AAAAACCAAAGTATTGATAAAAAAAA

FIGURE 6

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYEQDLCCRGRADDC
ALPYLGAIKYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLLAGWEQRLLGHDPG
```

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209,
296-300, 411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGACACATNACGCCGTCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTCGCTGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAAATGGCCCTGTCCAAGCCCTATGGAGG
TGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACC^{GCG}CATCCGCGCAGTTGCCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTCTGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGT^{CCCC}AAGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGAGCCTGTCCTGGTCCTGAGGCACATCTAACGAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCC^{TGAC}CCCTGCAGATGGCCCTCCAACCCCTCTGCTGGTGTTTC
CATGGCCCAGCATTCTCCACCCTTAACCC^{TG}CTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCCACCCATCTATGACTGAGCCAGGTCTGGTCCGTGGTCCCCGCACCCAGCA
GGGGACAGGCACTCAGGGGGCCAGTAAAGGCTGAGATGAAGTGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA
GGGCCAGGCCTCACATTCGTGGGCTCCCTGAATGGCAGCCTGAGGCACAGCGTAGGCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSDT
DPPADGPSNPLCCCFHGPADFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALR
RAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACCGTCCGAAACCTCTCCAGCGGATGGGAGCCGCCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTCAGGTCACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGGAAGCCCAGCAGGGAAAGAGCAAAGACTG
CGTGGTTCACGGAGATCGTGCTGGAGAACAACTATACGGCCTTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCGGCAGGGCGGCCAGGCTTCCGCAGCCGCCAGAAC
CAGCGGAGGCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTCCCCAACCACGC
CGAGAACGCAGTCGAGTTGTGGCTCCGCCCCACCCGCCGGACCAAGCGCACAC
GGCGGGCCCCAGCCCTCACGTAGTCTGGAGGCAGGGGCAGCAGCCCTGGCCGCCTCCC
CACCCCTTCCCTCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGCCAGATCCCC
GAGGGGAGGACCCCTGAGGCCGCAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGTG
CCCCAGGGCGGCTGGCACAGTGCCCTTCCGGACGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTCACCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC
CGCTGAAAGGTAGCGACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCCTAAAA
TCTGCTTCGGATCTCCCTCAGTCTGCCCCCCAGCCCCAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTCAGGAAAAAGAAAGGGAGAGAGAGAGGAAATAG
AGGGTGTCCACTCCTCACATTCCACGACCCAGGCCTCACCCCCACCCCAACTCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLISETDTFGSRVRIKGAESEKYICMNKRKGKLIGKPSGKS KDCVFTEIVLE
NNYTAFQNARHEGWFMAFRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQQQEF
VGSAPTRRTKRTRRPQPPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCGCACATGGAG
GACAGCAGCAAAGAGGGCAACACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTAGCTGGAGTTCTGGACTTCACAGAACCCCATTCCAGT
CATTTGATTTGCTGTTATTTTTCTTTTCTTTCCCACCAATTGTATTTAT
TTCCGTACTTCAGAA**ATGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTCCCT**
GAAGTCTTGGCTTATCATTCCCTGGGCTCTACTCACAGGTGTCAAACTCCTGGCTGCC
CTAGTGTGTGCCGCTGCCACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACAAATTATAATGC
TGGATTTCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTCCAAAGAATGTCAGAGTCTCCATTGCAAGAAAAC
AATATTCAAGACCATTACGGGCTGCTCTGCCCAGCTCTGAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAACCTGAGCAGTGTGCCTGTTGGCTTCCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCTATCCGACATGGCCTCCAGAA
TCTCACGAGCTTGGAGCGTCTTATTGAGCAGGGAACCTCCTGACCAACAAGGGTATGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTAACGTAATTGCTGTCC
CACCCCTCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCAAGAT
AAACCACATTCCCTTGACAGCCTCTCAAATCTCGTAAGCTGGAAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGTTTGATAATTCTCTCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCTGGTTGTGACTGCAGTATTAAATGGGTACAGAACGGCTCAA
ATATATCCCTTCATCTCTCAACGTGCGGGTTTCATGTGCCAAGGTCTGAAACAAGTCCGGG
GGATGGCCGTCAAGGAATTAAATATGAATCTTGTCCCTGCCCACGACCCCCGGCCTG
CCTCTCTCACCCCCAGCCCCAAGTACAGCTCTCCGACCACCTCAGCCTCCACCCCTCTAT
TCCAAACCTAGCAGAACGCTACACGCCTCCAACCTTACACATCGAAACTTCCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGACCCCACCTATTCTGAACGGATCCAGCTCTATC
CATTGGTGAATGATACTTCATTCAAGTCAGCTGGCTCTCTCACCCTGATGGCATA
CAAACTCACATGGGTAAAATGGCCACAGTTAGTAGGGGCATGTTCAAGGAGCGCATAG
TCAGCGGTGAGAACGCAACACCTGAGCCTGGTTAACCTAGAGCCCCGATCCACCTATCGGATT
TGTTAGTGCCACTGGATGCTTTAACCTACCGCGCGTAGAAGACACCATTGTCAGAGGC
CACCAACCATGCCTCTATCTGAACACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT
GTGCTGGTGGTCTGCTAGCGTCTTGTGGCATATGCACAAAAGGGCGCTACACCTC
CCAGAAAGTGGAAATACAACCGGGCCGGCGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACCAAGTTTCAGATCGTCTCCTAAATAACGAT
CAACTCCTAAAGGAGATTCAGACTGCAGCCATTACACCCAAATGGGGCATTAATTA
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACACAGCAGCGTGCACACCTGGAGC
ACTGCCATACGT**GACAGCCAGAGGCCAGCGTTATCAAGGGGACAATTAGACTCTTGAGAA**
CACACTCGTGTGTGCACATAAGACACGCAGATTACATTGATAATGTTACACAGATGCAT
TTGTGCATTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAAAGTG
CTATCTTCTATTCAAGTTAACAGTTGTAACCTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGAFFLKSLLIIISLGLYSQVSLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPaelHNvQSVHTVLYGNQLDEFPMNLPKNRVLHLQENNIQTI
SRAALAQLLKLEELHLDNSISTVGVEDGAFREAIISLKLFLSKNHLSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELNMNLLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPPTSKLPTIPDWDRGRERVTPPISERIQLSIHFVND
TSIQVSWLSSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNYRAVEDTICSEATHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQWKYNRGRRKDDYCEAGTKKDNSILEMTETSQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639,
649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602,
651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGCGGCCGGAGACAGAGGCAGAGGCAGAGCAGCTGGGCTCCGTCTCGCCTCCCACGAGC
GATCCCCGAGGAGAGCCGCGGCCCTCGCGAGGCCAGAGGCCGACGAGGAAGACCCGGTGGCTGCCCTCTG
CCTCGCTTCCCAGGCAGGCCGGCTGCAGCCTGCCCCCTTGTGCTGCCCTGAGGCCAGGGAGCGGTACGTGGAGGTCC
GCTGTTCTGCTGATCCTCGGACAGATCGTCCCTCCCTGCCAGACAGCAGCTGGAGAGTCTCTGTGAGAACAAAGCAGGGC
ATCTCTAGGGCAGACACGCTCGGACCCACCGCAGACGGCCCTCTGGAGAGTCTCTGTGAGAACAAAGCAGGGC
AGACCTGGTTTCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCG
TGGACATCTGCAATTCTTGACATTGGCTCTGATGTCACCCGAGTGGGCTGCTCCAATATGGCAGCACTGTC
AAGAATGAGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGAGGATGCCGATCT
GTCCACGGCACCATGACTGGCTGGCATCCAGTATGCCCTGAACATCGCATTCTCAGAACAGCAGAGGGGCC
GGCCCTGAGGGAGAATGCCCACGGCTATAATGATCGACAGATGGGAGACCTCAGGACTCGTGGCCAG
GTGGCTGCTAAGGCACGGACACGGGATCCTAATCTTGGCATTGGTGTGGCCAGGTAGACTTCAACACCTT
GAAGTCCATTGGGAGTGGAGCCCATGAGGACCATGTCCTTGTGGCCATTTCAGCCAGATTGAGACGCTGA
CCTCGTGTCCAGAAGAAGTTGTGACGCCACATGTGAGCACCCCTGGAGCATAACTGTGCCACTTCTGC
ATCAACATCCCTGGCTCATCGTCTGAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAG
AATCCAGGATCTGTGCCCCATGGAGGACCAACTGTGAGGAGCTCTGTGTGAATGTGCCCCCTCTCGTCT
GCCAGTGCTACAGTGGCTACGCCCTGGCTGAGGATGGGAGAGGTGTGGCTGGACTACTGTGCCCTAGAA
AACCACGGATGTGAACATGAGTGTGAAATGCTGATGGCTCTACCTTGGCAGTGGCATGAAGGATTGCTCT
TAACCCAGATGAAAAAACGTGACAAGGATCAACTACTGTGCACTGAAACAAACCGGGCTGTGAGCATGAGTGC
TCAACATGGAGGAGAGCTACTACTGCCGCTGCCACCGTGGTACACTCTGGACCCCAATGGCAAAACCTGCA
CGAGTGACCACTGTGACAGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACCGGAGGATTCTCGTCTG
CCAGTGTCTAGAAGGCTTCTCATCAACAGGACCTCAAGACCTGCTCCGGTGGATTACTGCTGCTGAGTG
ACCATGGTTGTGAATACTCCGTGTCACATGGACAGATCTTGGCTGTCACTGGGACACGTGCTC
CGCAGCGATGGGAAGACGTGTCAAAATTGGACTCTTGTGCTCTGGGGACACGGTTGTGAACACATTGTTG
AAGCAGTGAAGATTGTTGTGCCCCAGTGTGTTGAAGGTATATACTCCGTGAAGATGGAAAAACCTGCA
GGAAAGATGCTGCCAAGCTATAGACCATGGCTGTGAACACATTGTGTAACAGTGCAGACTCATAC
GAGTGCTTGGAGGGATTCCGCTCGCTGAGGATGGGAAACCGTCCGAGGAAGGATGCTGTCAA
CCATGGCTGCAACACATTGTGTTAATATGGAAATTCTACATGTCACAGGGGATTGGTTCTAG
CTGAGGAGCGGAAGACGGTGCAGGAAATGCACTGAAGGCCCAATTGACCTGGTCTTGTGATGGATCCAAG
AGTCTGGAGAAGAGAATTGAGGTGTCAGGAGTGGGAAACAGTCCACACAGAGTTCACTCTGAGAAACTCA
CAAAGCCGCTGAGTGGGCTGCTCCAGTATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTCA
CAGCCAAAGACATGAAAAAGCCGTGGCCACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCC
AAACACATGTTGAGAGAAGTTTACCAAGGAGAAGGGCCAGGCCCTTCCACAGGGTGGCCAGAGCAGC
CATTGTGTTACCGACGGACGGCTCAGGATGACGTCTCCAGTGGGCAAGTAAGCCAAGGCCAATGGTATCA
CTATGTATGCTGTTGGGTAGGAAAGCCATTGAGGAGGAACATACAAGAGATTGCCCTGAGGCC
CATCTCTTCTATGCCGAAGACTCAGCACAATGGATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGA
TCTAGAAGACTCCGATGGAAGACAGGAACCTCCAGCAGGGGAACGTGCAAAACGGTCAACAGCA
CTGAGGCCAGTCACCATAAATATCCAAGACCTACTTTCTGTTCTAATTGCACTGCAACACAGATATCTGTT
GAAGAAGACAATTGTTACGGTCTACACAAAGCTTCTCCATTCAACAAACCTCAGGAAGGCCCTTGG
AAAACACGATCAAGCAATGTGAAAACCTTATAATGTTCCAGAACCTTGCAACAGAAGAAGTAAGAAA
CACAGCGCTTAGAAGAAGAACACAGAGAATGGAAGGCCCTGGAAAATCGCTGAGATACAGATGAAG
ATCGCGACACATTGTAGTCAATTGATACGGATTACAATGAAACGAGCAGTGCAGAGGCCCAAGCTCAG
GTTAAATCAAAATGTTGTGAGTAAACAAATCAGTACTGAGAAACCTGGTGTGGCCACAGAACAA
GACAAGAACAGTCAACTGTTACGGTCTACACAAAGCTTCTCCATTCAACAAACCTCAGGAAGGCC
GTATACACTAATTGTATAAAATTCTAGGAAAAAAATCTTCAAGAATTCTAAGATGAATT
ATGAAAGCTATGCAAGGTATTGTAATATACTGTGGACACAACCTGCTCTGCTCATCTGC
GCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACTTCTGTAGAACACTGCC
TTTTTGTACTGGACTTTACCTGATATATGTATATGGATGTATGCATA
GAACAAAGTGGATTTTTACAAATATAAAATTCAACACTTCAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPOQTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIVGVQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINI PGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPVGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSRGKTCALKDSCALGDHGCE
HSCVSSEDFVCQCFCFGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFR
LAEDGKRCRCKDVCKSTHGCEHICVNNNGNSYICKCSEGFLVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDS LTISPKAARVGLLQYSTQVHTEFTRLRNFnSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAI VFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEDNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227,
243-247, 401-405, 442-446, 501-505, 624-628, 673-677, 706-710,
780-784, 781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459,
494-500, 639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423,
458-464, 540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCGCACGCTCCGCCGTCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGGCCCTGACTCCGTCCGCCAGGGAGGGC
CATGATTCCCTCCGGGGCCCTGGTACCAACTTGCTGCGTTTTGTTCTGGGCTGA
GTGCCCTCGGCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCGCCAACGGTGCAG
GCGGTGGAGGGAGGGAAAGTGGTCTCCAGCGTGGTACACCTGACGGGAGGTGCTTC
ATCCCAGCCATGGGAGGTGCCCTTGTATGTTCTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTCACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCTGCGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGCCACAGCATAAAACCT
TAGAACTCAATGTACTGGTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCAAATACCA
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTCACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCAGGCCCAC
AATGAGGTGGGACTGCCAATGTAATGTGACGCTGGAAAGTGAGCACAGGCCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGTACCCCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCACCGCCGGGCAAGGCCCTGGAGGAGGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCC
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCATGGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCCTCTGGCTTGAGCCG
CATGGGTGCTGTCCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**GATGAC**
CCCACCACTATTGGCTAAAGGATTGGGCTCTCCTCTATAAGGGCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCTCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAAATCTC
TTATTAAAACATGAAATATGTGTTTTCTTGCAAATTAAATAAGATAACATAA
TGTTTGATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSKP
AVQYQ WDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGT
AQCNCVTLEVSTGPGAA VVAGAVVGT
LVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIA
PRTLPWP
KSSDTISKNGTL SSVTSARALRPPHGPPRGALTP
PSLSSQALPS
PRLPTTDGAHPQP
I
S
P
I
PGGVSSSGLSR MGAVPVMVPAQS
QAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258,
256-262, 262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCAC TGCGGCCACCGCCAATGAAACGCCTCCGCTCTAGGGTTTTCCACTTG
TTGAATTGTTCTATACTCAAAATTGACCCAAGACACCTTGTCTCCAAATGCAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCCTGTGGCAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA
AGACAGGTTACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGCCATT
TAGATAATGTCTGTATAGCTGCAAATATTAAATAAAAATTAACTGACAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAAGAAATATTAGCTGAATCATCTTCAATTACTAGGTTACAAGAACACA
CTATCTCAGCCAAGGACACCCTTCTAACACTCTTACTGAATTGTAACCGTGAAT
AATTGTTCAAAGGGATACATTGTAGTTGGACAAGTTCTGTGAATCATAGGAGAAC
ACATCTACAAAACATGCACACTGTTGAACAAGCTACTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTCTTTTGAT
TCATATAACATGAAACATATTCTCCTCATATGAATATGGATGGAGACTACATAAATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATT
AGAGTATTGGTCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATGAACCTGAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCATTGGATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTTGCAATTGGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATT
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGTTGCTTGCATATGCATT
ACCTTCTGGTTCTCAGTGAATTCAAAGCACCAGGACAACAATTCAACAAAATCTTGCTG
TAGCCTATTCTGCTGAACCTGTTCTTGTGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATGCCGGACTGCTACACTACTCTTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCATACATCTATCTCATTGTTGGTGTCACTACAACAAGGGATTTGCA
CAAGAATTATTTATATCTTGGCTATCTAAGCCCAGCCGTGGTAGTTGGATTTGGCAGCAC
TAGGATACAGATATTATGGCACACCAAAAGTATGTTGGCTAGCACCAGAAACACTTATT
TGGAGTTTATAGGACCAGCATGCCCTAACACTGCAGGGTTGAAACCAAGAAGTTAGTTGCTTGGAGTCAT
CATATACAAAGTTTCTGTCACACTGCAGGGTTGAAACCAAGAAGTTAGTTGCTTGGAGAACA
TAAGGTCTTGCAAGAGGAGCCCTCGCTCTGTTCTCTGGCACCACCTGGATCTT
GGGTTCTCCATGTTGCAACGCTACAGTGGTTACAGCTTAACCTCTCACAGTCAGCAATGC
TTTCCAGGGATGTTCAATTCTTATTCTCTGTGTGTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTCAAAATGCCCCGTTGTTGGATGTTAAAGGTAAACATAGAGAATG
GTGGATAATTACAACCTGCACAAAATAAAATTCCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCCAATTATTAACACTAGACAAAAGTATTAACTCAGTTTCT
GTTTATGCTATAGGAACTGTAGATAATAAGGTTAAATTATGTATCATATAGATAACTATGT
TTTCTATGTCAGGAAATGTTCTGTCAAAATAGTATTGCAAGATATTGGAAAGTAATTGGTT
CTCAGGAGTGTATCACTGCACCCAAGGAAAGATTCTCTAACACGAGAAGTATATGAA
TGTCTGAGGAAACCACGGCTGATATTCTGTGACTCGTGTGCCTTGAAACTAGTCC
CCTACCACCTCGGTATGAGCTCATTACAGAAAGTGGAACATAAGAGAATGAAGGGCAGA
ATATCAAACAGTGAAGGAAATGATAAGATGTATTGAACTGTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAAACACATTACCAATTGAA
TTGTTCTGAACCTAAATGTCCACTAAAACAACAGACTCTGTTGCTAAATCTGTTCTT
TTCTAAATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSNQDRFITNDGTVCIENVNANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTEFVKTVNNFVQRDTFVWDKLSVNHRTHLTLMHTVEQATLRISQSFQKTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSRKVTDRYRSLCAF
WNYSPDTMNGWSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTWFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGL
LHYFFLAFAFWMCIEGIHLYLIVGVLYNKGLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLVVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593,
619-636, 648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCTTGTTCATCATCTGACAACCTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACCTGAAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCTCCCAGATCCGAACGGCCTGGCGGGTCACCCGGCTGGGA
CAAGAACCGCCGCCTGCCCTGCCGGGGCCGGGGAGGGGGCTGGGGCTGGGCCGGAGGC
GGTGTGAGTGGGTGTGTGCGGGGGCGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTGGGCACCTACCCGTGGGCCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGCCCGCGCCGTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCACGACCATCCAAACCC
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGGCCAGCCTCCGCACCCCCATGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATCGGAGCGGGTGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCCCGCCCTCGCCTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGCCACCCCATCCGCTGCGCACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTTCTGCGATCCGTGCCGACGGCGTGTGGACTGCGCGGGGGC
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCACGGCAAGATGCAGGCCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAACGACCGCCTCCGGTCTCCCTGAGCAGTGCACAGGGAGCTGTACAAGAA
CAGAGGCTTCTCCACTCTCATTTCTGCCATGCTGCCCATGGTCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTCTGCCCTGGAGACCGACAGCATG
GACCCATTGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAGTAACT
GAGACCATGCCCGGGCTCTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCAGTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCCCTGGGCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTGAATACCTCATCGATGGGAAC
TCACCTCCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTCTCATCACTTC
CCCAGGAGCAGCCAGAACAGACAGGCAGTAGTTAATTCAAGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTCACTCAACCCATGTGGATTGATCTATCTACTTCCAGGG
ACCATTGCCCTCCAAATCCCTCAGGCCAGAACACTGACTGGAGCAGGCATGCCACCAG
GCTTCAGGAGTAGGGAAAGCCTGGAGCCCCACTCCAGGCCCTGGACAACTTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTTGAGAATAACTTGCTGTCCGGTGTACCTGC
TTCCATCTCCAGCCCACCAGCCCTGCCCCACTCACATGCCCTCCCATGGATTGGGCCT
CCCAGGGCCCCCACCCTATGTCAACCTGCACTTCTGTTCAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCAATAACTTGCTGTGGAAAGCAGCGGGGAAGACCTAGAAC
CCTTTCCCCAGCACTTGGTTTCCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTTCTTACATTATTATGCCCAAATTATTTATGTATGTAAGTGAGGTTG
TTTGTATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEET
EIRPDGYNVYRSEKHLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLES
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGGAAGATGGCGAGGAGGCCACGCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCCAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA
AGAAGACTGTTCTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTCCTTGCTAC
TATCAACAGACTCTTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAAATGTGACAAGAAGTGTGAGCTGGGGAAATATCGTTGTGAAGTTAGTGGCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATAACAGTCACCTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAATCCAGCTCCTGAATAACACATGGTTAAGGATGGCATCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAAC
CTGCAATTAAACTGTTCAAACGGACACTGGAGAATATTCTGTGAAGCCCGCAATT
TGTTGGATATCGCAGGTGTCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTCCGTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTAAAATGTGCAGTGGCTACGCCTGTAATCCCAGCAGTTGGAAGG
CCGGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTAAACCC
CATCTCTACTAAAATACAAAATTAGCTGGCATGGTGGCATGTGCAGTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAATA
AATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLRYLVVALGYHKAYGFSAPKQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD GIRLLENPRLGSQST
NSSYT MNTKTGTLQFNTVSKLDTGEYSCEARN SVGYRRC PGKRMQVDDLNI SGIIIAVVVVA
LVISVCGLGV CYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRQ
EF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATAACATGCTCCACAGCCCAGCCCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAACATGGGATTAAATATTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCACATCTACATACTCCACCTTCAGGAAAGTACATCAATA
TTATATCATTAGGAAATAGTAACCTCTTCTCCAATATGCATGACATTGGACAAATG
CAATTGTGGCACTGGCACTTATTCACTGAGAAAACCTTGTGGTCTATGGCATTCA
TTTGACAAATGCAAGCATCTCCTATCAATCAGCTCTTGAACCTACTAGCACTGACTG
TGGAAATCCTTAAGGGCCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCACTGTGCTACTTGGCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAAGTCTCCAGGCCAGATTGCC
AGCTAACACACAGATTCTCTCCTACAGACTAACAAATATTGCAAAATATTGAATACTCCACAG
ACTTTCCAGTAAACCTACTGGCCTGGATTATCTCAAAACAAATTATCTCAGTCACCAAT
ATTAATGTAAGGAAAGATGCCCTCAGCTCTTCTGTGTACCTAGAGGAAAACAAACTTACTGA
ACTGCCTGAAAATGTCGCTCCAACTGAGCAACTTACAAGAACTCTATATTAACTCACAACT
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTCTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTTTATCA
ATCTTCGCAGCCTGGTTAGCTGGTATAAACCTCACAGAAATACCAAGATAACGCCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTACGATAACAGGTTATTAAAGTACCCCATGT
TGCTCTCAAAAAGTTGTAATCTCAAATTGGATCTAAATAAAATCTTAAATAGAA
TACGAAGGGGTGATTAGCAATATGCTACACTTAAAGAGTTGGGATAAATAATAGCCT
GAGCTGATTCCATCGATAGTCTGCTGGATAACCTGCCAGATTAAAGAAAATAGAAGC
TACTAACAAACCTAGATTGTCTTACATTCCCCAATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCATGGTACTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCATCAGGTGTACTGTGTCATCCGTTG
GATGAACATGAACAAAACCAACATTGATTCTGATGGAGCCAGATTCACTGTTTGCCTGGACC
CACCTGAATTCCAAGGTAGAAATGTTGCCAGTGCATTCAAGGGACATGATGGAAATTG
CTCCCTCTTATAGCTCTGAGAGCTTCTTCTAAATCTAAATGTAGAAGCTGGGAGCTATGT
TTCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACCTTGCCTAATACCCGTACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA
GATATAAAATGGCGTAACCTCCAAAGAAGGGGTTATATACTTGATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAAATG
GCTCTTGAATATTAAAATAAGAGATATTCAAGGCCATTCAAGTTGGTGTCTGGAAAGCA
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTGCGCAAAGTGTGCAATACCATCTGATGTCAAGGTATATACTTACTCATCTGAATC
CATCAACTGAGTAAAAATTGTATTGATATTCCACCATCTACAGAAAACAGAAAAAAA
TGTGTAATGTCAACCACCAAGGTTGCACCCGTACAAAAGAGTATGAAAAGAATAATAC
CAACACACTTATGGCCTGTCTGGAGGCCTCTGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACCTGTGATGGTGGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCCTGTGATAATCTCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCC
AAAAACCAACCAAGGAAACCTACTCCAAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVKDCPRLCTCEIRPWFTPRS IYMEASTVDCNDLGLLT
FPARLPANTQILLLQTNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLSNRQLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVVLNKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDS LAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNAL S A LY HGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNI RFM EPDSLFCVDPPFQGQNVHQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTL DINGVTPKEGGLYTC
IATNLVGADLKSVMIKV DGSFPQDNNGSLNIKIRD IQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVN VTTKGLHPDQKE
YEKNNTTLMACLGGLLGIIGVICLISCLSPEMNC DGGHSYVRNYLQKPTFALGELYPP LIN
LWEAGKEKSTS LKV ATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526,
579-583, 608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGGAGTAGATGAGGAATGGCTCGTATTGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTGTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAACTCTGGACTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAACACGTCCGTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTGGCTGGTCACTATGGTATCTCATATGTGGTATATTATGTGAGGAAAATCAGGAG
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTCTCCCATCCATTGTAAACATTGAA
ACTTTGTATTCAGTTTTGAATTATGCCACTGCTGAACCTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAA
ACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMC PKGCLCSSSGGLNVTC SNANLKEIPRDL
PPETVLLYLDNSQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNICKTSVLDEHAGR PFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCCGCCCAGATGCAGGTGAGCAAGAGGATGCTGGCGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT
GGGCTCAGTGCTTCAGGCTCGGCACGGCTGCCGCCCCGCTGCAGTGCTCCGCCAGG
ACCGCGCTGTGCTGCCACCGCAAGTGCTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCTGCTGGACCTAGGAAGAACCGCATAAAACGCTCAACCAGGACGAGTTGCCAG
CTTCCCGCACTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGGCCGTGGAGGCCGG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCCGCTGAAGCTCATC
CCGCTAGGCTGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTCAAGGACCTGTACAACCTCAAGTCACTGGAGGTTGG
ACAATGACCTCGTCTACATCTCACCGGCCTTCAGCGGCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCTGTCCCACCTGCACGGCCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCTACTGGACACCATGACACCCAAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCGTCCGCCACCTAGTCTATCTCGCTTCCTCAACCTCTCCTACAACCCCATCA
GCACCAATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGG
GGGCAGCTGGCGTGGTGGAGCCCTATGCCTCCGGCCTCAACTACTCGCGGTGCTCAA
TGTCTTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCTCGACTGTCGGCTCTGTGGGTTCCGG
CGCCGCTGGCGGCTCAACTCAACCGGAGCAGCCCACGTGCCACGCCAGTTGTC
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGTACTGCCAACTACTTCACCTGCCCGCG
CCCGCATCCGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGGCACACGGTGCAGTTT
GTGTGCCGGCCGATGGCACCCGCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCTGATGGCACGCTGGAGGGTGCG
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCTCGCCAACGCCGGCGAACGAC
TCCATGCCGCCACCTGCATGTGCCGACTCGCCGACTGGCCCCATCAGCCAAACAA
GACCTCGCTTCATCTCAACCAGCCGGCGAGGGAGAGGCCAACAGCACCGGCCACTG
TGCCTTCCCCTCGACATCAAGACCTCATCATGCCACCAGGCTTCATCTCTTC
CTGGCGCTGTCTTCTGCTGGTCTGTTCTGGAGCCGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCGAAGTCGGACGAGGCATCAGCTCCGCG
ACGCGCCCCGCAAGTTCAACATGAAGAGTTATTGAGGCCGGGGCGGGGGCAGGGACCCCG
GGCGGCCGGCAGGGGAAGGGCCTGGTCCCCACCTGCTCACTCTCCAGTCTTCCCACCTC
CTCCCTACCCTCTACACACGTTCTTCTCCCCCGCTCCTGTCCCCTGCTGCCCC
CCAGCCCTACCACCTGCCTCTCCTTCTACCGACCTCAGAAGCCAGCTGGGGACCCCA
CCTACACAGGGCATTGACAGACTGGAGTGAAGGCCGACCACGCGGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACTTCTGTACTTGGTTTCAATAATTATGGATTT
TATGAAAACTTGAAATAATAAAAAGAGAAAAACTAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL
GLRSNRKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKMLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFNLNSYNPISTIEGSMHLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTTLEESVFHSVGNLETLLIDSNPLA
CDCRLLWVFRRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297,
341-345, 492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352,
349-353, 607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACCGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGCGCCCTTCGGTCAAC
ATCGTAGTCCACCCCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGCGCCCAGCC
AGGGAGCCGGCCGGAAAGCGCGATGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC
TGTTGCCTGCTGCTGGCGCCCGGGCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGCACCGTGGTCAAGTCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTACTTGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCAAGCTGGTTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACCCATCATCACTGGTT
ATAAAATCTTCATTACGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGAGCAAG
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTACCAAGAACCTCCACGGAGAACCAACCCGAT
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT
CCTCCTCCAGCACCTACCACGCCATCATCGTGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCCAGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGAGCACAAGAAGGAATATTCATCTAGAGGCCTGCCACTCCTGC
GCCCCAGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCGTACAGAATGTCTGC
TTGGGTGCGTTTGACTCGGTTGGAATGGGAGGGAGGAGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGTGAGAAAAGCAAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFAACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACTTGAATTGTGCTGTCGCCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAAATGCTGCTTGGATTCTGTT
GCTGGAGACGTCTTTGTTGCCGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCAGTAACTTACCTTATTCTGCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTTGCTAACATTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGATGAAATCGTCCGGGGCTTTCTGGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTCAAGAACAGACTTTCTGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTAAATTATTACGAGATATAGACCCGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
GTGTTCCAGTATGTGCCATCACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT
GGGACTGCACCTGTGATCTGCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGCTTGAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG
CCCAAGAACAGAGACCTTGCTCCTGGACCCCTGCCAACCTTCAAGACAAATGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACCGTAGCTCAGGAACAAACCTTAGCTAAC
GTTTACCCCTGCCCTGGGGCTGCAGCTGCACCACATCCAGGGTGGTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGAGGA
GCTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGACTTGTGGATTACAAGA
ACCTCATTCTGTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCGGGA
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGGACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTAACAAACAACCTG
CTGAGGTCCCTGCCTGGACGTGTTCGCTGGGCTCGCTCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACAGCTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGTGCTGCACAATTGTGCCCTTCAAGCAGTGGCA
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTT
TAGAAAGGATTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACTTCGACAGTAAAACAGCACTGGGTTGGCGGAGACCGGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTGGTCCGGGACTGCTGTT
GTTGTCACCTCGCCTCACCGTGGGGCATGCTCGTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGAGCGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTGT
GACTCTCCTACTGGCACAATGGCCTTACAACGAGATGGGCCAACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAGACCCAAACCCAAATAGGGAGGGCAGAGGGAGGG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCCGCG
CCATCAGCCTGGATGGCATAAGTAGATAATAACTGTGAGCTCGCACAACCGAAAGGGCCT
GACCCCTTACTTAGCTCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGGCCCTTGACAGAAAGCCAGCACGACCCCTGCTGGAAG
AACTGACAGTGGCCTCGCCCTCGGCCCCGGGGCTGTGGGGTTGGATGCCGCGTTCTATAC
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTTCCTCTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGATGGGAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSCLCFAAGNVTGVCCKICSCNEIEGDLHVDCEKKGFTSLQRFTA
P TSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLEVLI
LNDNLISTLPANVFQYVPITHDLRG
NRLKTL PYEEVLEQI PGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSL PAPPAQEETFAPGPLPTPKTNGQEDHATPGSAPNGGT
I PGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSDHI PGSGLKMCNNRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNALIQLI
LPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNYYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSKNSNSTGLAETGTHNSYLDTSRVSISVL
VPGLLL VFTSAFTVVGMLV FILRNRKRSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370,
573-577, 608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTCTGTGCGGCCCTAACGGAAACTGTTGGC
CGCTGGGCCCGGGGGATTCTGGCAGTTGGGGTCCGTCGGGAGCGAGGGCGGAGGG
AAGGGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCAGCCTCCAGACAC
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGAGCAGCTCTGCGTGCAGGGCCTCAG
AGAATGAGGCCGGCGTTCGCCCTGTGCCCTCTGGCAGGGCTCTGGCCGGCG
CGCGAACACCCCCACTGCCGACCGTGCTGGCTGCTCGGCCCTGGGGCCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGCGCTC
AGCACCGTGCCTGGGGCGCGAGCTGCCGCTGTGCTCGCGCTCCCTGCCAGGCCAGG
GCCCGGAGGGGCTCAAAGACCTGCTGTTCTGGTCGACTGGAGCGCAGGCCTCCACT
GCACCCCTGGAGAACGAGCCTTGCAGGGTTCTCCTGGCTGCTCCGACCCGGCGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCTGCACCGCGCGAGATGCGC
GGTACTCCAGGCCACCAGTGGGTCGAGCCCGCAGGCTGGAAGGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTTGTGCTCGGCCGCCCCGGG
GCCGCCTCTAACTTGAGCTATCGCGCCCTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCGCCGGGACAGCTCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGCTCCCTGCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCTAACTGCCTAGACGACTTGGAGG
CTTGCCTGCAATGTGCTACGGCTTCGAGCTGGGAAGGACGGCCGCTTTGTGACCA
GTGGGAAGGACAGCCGACCCCTGGGGGACCGGGGTGCCACCAGCGCCGCCACT
GCAACCAGCCCCGTGCCAGAGAACATGGCAATCAGGGTCGACGAGAACGCTGGAGAGAC
ACCACTGTCCCTGAACAAGACAATTCAAGTAAACATCTATTCTGAGATTCTCGATGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGTCCTCAAGCCAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTCCTCTGCCACTCCTCAGGCTT
CGACTCCTCTGCGCTGGTCTCATATTGTGAGCACAGCAGTAGTAGTGTGTTGATCT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAAGAACGGCCCTTCCAGCCA
AGGAAGGAGTCTATGGGCCGCCGGCTGGAGAGTGTACCTGAGCCGCTGTTGGCTC
CAGTTCTGCACATTGCAAAACAATGGGTGAAAGTCGGGACTGTGATCTGCGGACAGAG
CAGAGGGTGCCTGCTGGCGAGTCCCTCTGGCTCTAGTGATGCA**TAGGAAACAGGGAA**
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTTCCCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAC
TGGTGATAGTGGGGACCGGGTAGTGCTGGGAGAGATATTCTATGTTATTGAGAA
TTTGGAGAAGTGAACATTCAAGACATTGAAACAAATAGAACACAATATAATTACA
TTAAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTCGAAATCCCAGGGAAAAAATAAAATAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPG
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACCGCGTGGGATTCAAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATACTGCCTTAAAGTGCCTCCGCCCTGCCGGCCCGTATC
CCCCGGCTACCTGGGCCCGCCCGCGCGTGCAGCGCTGAGAGGGAGCGCGGGCAGCGA
GCGCCGGTGTGAGCCAGCGCTGCCAGTGTGAGCGCCGTGTGAGCGCGTGGGTGCGGA
GGGGCGTGTGCGCCGGCGCGCCGCGTGGGTGCAAACCCCGAGCGTACGCTGCCATGA
GGGGCGCAACGCCCTGGCGCCACTCTGCCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTCTGGAGTGACCCCTCAAATAGCAAATGTACTTGGAAAATCA
CAGTTCCCAGGAAAAGTAGTCGTTCTCAATTTCGATTCAAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTGTGGATGTGTACAATGCCATGCCATGGCCAGCGCATTGGCCG
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTTATGCCATGTTCTCCGCTGCTGAACCA
AACGAAAAGAGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTCCGGCTTTAAAAC
CCCCAACTGGCCAGACCGGGATTACCTGCAGGAGTCATTGTGTGGCACATTGTAGGCC
CAAAGAACATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGGGGGAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGTAGTCCACCTGCAGCAATTGTGTCTGAGAGAAATGAACTCTTATTCACT
TTTATCAGACTTAAGTTAACTGCAGATGGTTATTGGTCACTACATATTAGGCCAAAA
AAACTGCCTACAACACAGAACAGCCTGCAACCACATTCCCTGTAACCACGGGTTAAA
ACCCACCGTGGCTTGTGTCACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGAATTGTATTAGCCGGACTGTTATCACAAACATCACTCGCATGGAGTTG
CACGCCACAGTCTGATCATCACACATCTACAAAGAGGGAAATTGGCATTGAGCAGGGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGCTGCAAGCAGTGCCTCTCAGAAGAGGTC
TAAATTACATTATTAGGGCCAAGTAGGTGAAGATGGCGAGGCAAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCTCTGGATGCCAAAAATAAGCAATG
TAAACAGTGAACGTGTCATTAAAGCTGATTCTGCCATTGCCATTGCTTGAAGATCTATGTT
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGTTGACTCTCACATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAAAGTTCTT
TGCCTGCTGTCAGAGGAGCAGCTATGATTGAAACCTGCCACTTAGTGCCTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTATTATACATCTCTGAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTGTTAGAAGTGCATATTATAGT
GTTATTGTTCACCTCAAGCCTTGCCTGAGGTGTTACAATCTGTCTGCCTTCTA
AATCAATGCTTAATAAAATTGTTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPD RDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELL
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEG
YCSSDFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCCTGGCGGACCGCTGGCGGCCACGGCGCCCGGGCTGGGCGGTGCTTCTT
CCTCTCCGTGGCCTACGAGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGACAACTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGTCAGCAAGTCAGACTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCCCTGGGGAACAGAGAGGCCCTGCGGTGGCTACGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAACGCCAGCCATCTGGTATGTTGGCTTGT
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGAATGCAAGAAGG
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGG
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCA
ACTGAGGCTGACCAATTCTCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGGCCAGGTGCGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGGTGTCCGGGAGAGA
ACAAGCAGTGTAAAACACCGAGGGCGTTATCGCTGCATCTGCGCAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGCAGCAGATGTTGGCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCAGTTGGTGGTACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCGAGAGCTTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTGGTTATTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAGGAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCGCAGCTGCATGCTGCCAGTCCCTGT
TCTGTGTTACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPKGLVPAVLWGSLFLNLPGPIWLQPSPPPQQSSPPQPHPCHTCRGLVDSFNKGLERT
TIRDNFGGGNTAEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCPGGTERPCGGYQQCEGEGRGGSGHCDCQAG
YGGEACGQCGLGYFEAERNASHLVC SACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGMAGPGRKKCSPGYQQVGSKCLDVDECE
TEVCPGENKCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173,
173-179, 177-183, 188-194, 250-256, 253-259, 267-273, 280-286,
283-289, 326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCAGGGCA
GCACCATGCAGCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCGGAGCTGCAGCTCAAAGAGGT
GCCCACCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTGGAGGCCAGCACACACCTGCTGGTGGTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGGCTCTCCAGG
AGCCGGTCCCCAAGGCCCGCTGCACAGGCACGGCGGCTGTCCCCCGCGAGCGCCGGGCC
CGGGTACCGTCGAGTGGCTGCGCGTCCCGCAGCACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC
GCCAGCCGGCTGGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTGGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACTGGTGCTGGAGCCCCGGCTT
CCTGGCTTATGAGTGTGGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTCAAGTGGC
CGTTTCTGGGCCCTGACAGTGCATGCCCTGGAGACTGACTCGCTGCCATGATGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCCTGGATGGTGCCTCGTAAGTGGTCAAGTGGTACCAAGGAGAGCTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTCAAGTGGTACCAAGGAGAGCTG
GCGATGACTGAAGTGCATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGGCCACTGGA
GAGCCCTTGCTCAGTTCTATTCTATTACTGCACTATATTCTAACACTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGTCCGTAC
TGGATCTGGCTAAAGTCCCTCACCACCTGGACCTAACAGACCTGGGGTAAGTGTGGT
TGTGCATCCCCATCCAGATAATAAGACTTGTAAAACATGAATAAACACATTTTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFSREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGGGCTGTTGTCAGTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTCGCCTTCAATTGGCGATCCTGTTGCTCCCTGG
CATTGGGCAGTGTACAGTCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGGAGTGGAGTTGACCA
AGGAGACACCACCACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG
TGACCTTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGAAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCTGCCACCATTGGAACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATACACCTGGTCAAAGAT
GGGATAGTGATGCCCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTCCTATGTCCT
GAATCCCACAACAGGAGAGCTGGTCTTGATCCCCTGTCAAGCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCGTCTGTAACCCCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCATAGCCAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCCCTGGTGAGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCCTACT
CAGGTGCTACCGGACTCTGGCCCTGATGTCAGTTCACAGGATGCCATTGTCCTTC
TACACCCCACAGGGCCCCCTACTCTCGGATGTGTTTAATAATGTCAGCTATGTCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTTGTTAAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATTTGAATAGGTATCTTGAGCTGGTCTGGCTCTTCCTGTACTGAC
GACCAGGGCCAGCTGTTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGGCCTTCATCTCTGGGCCACTCTCTGCTTCCATGGGAAGTG
CCACTGGGATCCCTGCCCTGCTCCTGAATAACAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACTGAAGCCAAAAG
GATTAAAACCCTGCTCTAAAGAAAAGAAAAGCTGGAGGCTGGCGCAGTGGCTACGCCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTCAGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTCATGCCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIENNPKLSCAYSGFSSPRVEW
KFDQGDTTRLCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCEQDGSPPSEYTWFKDGI VMPTNPKSTRAFSNS
SYVLNPTTGEVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVI VAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243,
256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCCGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCGAGGCCAGCTCAG
GCTCGTGCACCCACCAAGTCCAGTGCCGACCAGTGGCTATGCGTGCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACGCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGAACTGACAAGAAACTGCGCAACTGCAGCCCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTGGCTGTGAAACCAATGAGATCCTCCCGAAG
GGGATGCCACAACCATGGGCCCTGTGACCCCTGGAGAGTGTCCCTGTGAGGATGTCACCTCTCAGGAATGCC
ACAACCATGGGCCCTGTGACCCCTGGAGAGTGTCCCTGTGAGGATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAATGCCTATGGGTTATTGCAGCTGCTGCCGTGC
TCAGTGCAAGCCTGGTACCGCCACCCCTCCCTTGTCCCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC
CTCGCTGCCTGAGGACAAGCACTTGCACCCCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGGATGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAAACCTGCCACAGCCAGAACAG
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDGSDEEECRIEPCTQKGQCPPPGLPCPCTGVSDCSGGTDKKL
RNCSRRLACLAGELRCTLSSDCIPLTWRCDGHPDCPDSSDELCGTNEILPEGDATTMPPVT
LESVTSLRNATTMPPVTLESVPSVGNATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172,
212-218, 224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCGAGCGGCCGCAGCAGAGGTGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTTCAAGTGTGCTGACCCGGCATTCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCA
ACAAGACATATAGACATGGAGAGAAGCTAACATCACTTGTCACTGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCCAATGGTAGTCACGGAGATTCTGTCT
GCCACCCCGGGCCTTGTGAGCGCTACAAACCACGGAACGTGGTGGAGTTACTGCGATCCT
GGCTACAGCCTACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCGGAG
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTGGCATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCTTAGGCCCGGTACATGGCTCTGTGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCACCCAGTGGCTCTGGACAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAGGAAACTTCCAAAGTGTCTGAAGTGTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTTGGTTTAGACAAATGTAAACAA
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTAAGGAAACTTAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKKGATKRLCLKHFNGLGWI PSDNS ICVQEDCRI
PQIEDAEIHNKTYRHGEKLI ITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPI CQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASDNPDI IASTAEEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCCCCTCGCTGCCAGGGTCCGTGGTGGCCTAGAGA
TGCTGCTGCCGCCGGTTGCAGTTGTCGCGACGCCCTGCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAACCGCGCTACAGG
CCGTGCTGCTGCCGTGCTGGTGGGGCTGCCGCCAGGGTCCGTGGTGGCCTAGAGTGCC
TCGGATTGGACCTCAGAGGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTGTTA
TAAAGTCATTTACTCCATGATACTTCTGAAGACTGAACATTGAGGAAGCCAAGAACGCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTCATTGAAAACCTTGCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCAGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
CACAATTAGGAACGGTATGTGGATGAGCCGTCCGCCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGATGATGA
CCGGTGCACATGAAGAACATTCATTTGCAAATATTCTGATGAGAACACCAGCAGTCCTT
CTAGAGAACGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAACACAG
GAAGAACGATGCCAAAAAACATTAAAGAAAGTAGAGAACGCTGCCTGAATCTGGCTACAT
CCTAATCCCCAGCATTCCCTCTCCTCCTGTGGTACCCAGCTGATGTTGGTT
GGATCTGTAGAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAAGGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAACGCTGACTTAGCTGAGACCCGGCAGACCTGAAGAATATTCAATTCCGAGTGTGTT
CGGGAGAACCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACAAATGGGGAGGAGTAAGGAGTCTGGATGGTGAAATGAAATATG
GTTATTAGGACATATAAAACTGAAACTGACAACATGAAAGAACGAAATGATAAGCAAAATC
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAAACAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCTGTTGGACCCACGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTCGACCTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAAAATGTCACTTGGTTGGTTGTATCTAACCTTAAGGGACAGAGCTTACCTG
GCAGTGATAAGATGGGCTGTGGAGCTTGGAAAACCACCTCTGTTCTGCTATACAG
CAGCACATATTACACAGAACGAAATCCAGAACATTCAAAGCCCACATATGGTAGCA
CAG
GTTGGCCTGTGCATCGGAAATTCTCATATCTGTTTTCAAAGAAATAAATCAAATAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIKEKFIENLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLL
VTTVVCWWICRKRKREQPDPSKKQHTIWPSPHQGNSPDLEVNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSFGVTLSVESGFVTNDIYEFS
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGTAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCGCAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGGCCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCATT
GCAGCAAATGTTGCCTTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTTGGAAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAAGTCTTGATCCAACTACCAAACCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCCTCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTCTATGCCGCTCATGATG
TGACCTTCATACCGCTTTAATGACCCCTGGGATTGGACCAAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAAATGCCATGTCAGTTATACCTTAAGCCCAGAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGCCTTATACAATG

BIOEDIT 7.0.9.5

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFIILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLIES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAAACATAATTCGCTGGGGACCTCCTTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGCCT
CCACCGCTGTGAAGGGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGCCACAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA
GTCCCAGAGGTGTCAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGAA
GCACCAGAACCAGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGCCAGATGTCATGCTCAGGACGAGAACCAACCTCA
GGATTGCCCTCTGGCCTGGGGAAAGAACACCTGCAACCATGATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGAACCTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGGTATGGGCTCTGTCTGTGATGACAACTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGCTGTGGAAAGTCCCTCTCCCTTCAGAGACCGGA
AATGCTATGCCCTGGGGTTGCCGCATCTGGCTGGATAATGTTGCTCAGGGAGGAG
CAGTCCTGGAGCAGTGCCAGCACAGATTGGGGTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAACACTGTTGAGTGCCTGAATAGAA
AAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTAAACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTCTCAGGCCATCAGACATAGTTGGAACACTACATCA
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTAT
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACACACATA
CACCATTGTCCCTGTTCTGAAAGAACTCTGACAAAATACAGATTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGATAAATTCTGAATTGGTATGGGTTCTGAAATTG
GCTCTATAATCTAACATTAGATATAAAATTCTGGTAACTTATTACAATAATAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGHLRCEGRVEEQKGQWGTVCDDGWDIKDVAVL
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQLMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104,
137-143, 180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGTCCCGGGACCGTGGCGGACCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCCGAATGCTG
TGGTGGTGATCACAGGCCACCTCAGGGCTGGCAAAGAAATGTGAAAAGTCTTATGCT
GCGGGTGCTAAACTGGTGCTCTGGCCGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGCATGGAGACAAACTACTTGGCCCAGTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCAAGGCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTGGCTGTTATCTCGAA
CTCTGGCTCCTGGCTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGTCTCACAAGTGGG
AAAGACTGAAGAAACACATCTGTCAGATCTGCTGGCAGAGGACAATCAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAGGCGGCCGACTCTAG
AGTCGACCTGCAGAAGCTGGCCCATGGCCAACTGTTATTGCAGCTTATAATGGTTA
C

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL
.VNNAGISYRGTIMDTTDVKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTCTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCGGCAGAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GACACTGACTGCCTATGAATTGCTAAACTAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAATGCAAGGGACTGGTGCCAGGTTCATACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACACATTCTGGACTACAAA
GGCATTCTTCCTGCAATGACGAAGAATAACCATGCCATTGTCACTGTGGCTCGGCAG
CTGGACATGTCTCGTCCCCTTACTGGCTACTGTTCAAGCAAGTTGCTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACTGGCTGCCTACAAATAACTGGAGTCAAAACACATG
TCTGTGTCCTAATTCGTAACACTGGCTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTCTATAGCTTTAAACAACATTGAAAGGATCCTCCTGAGCGTT
CCTGGCAGTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAATGA
AAGCGCAATAAGCACCTAGTTCTGAAACTGATTACCAGGTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTAAATGTTGAACTTCTGTTCTAATTATCCCCATTCTCAATA
TCATTGGAGGCTTGGCAGTCTCATTACTACCACCTGTTAGCCAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTAAGGAAATGAAGAAAAGAA
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGCAA
AATTGTACCATAACCGTTATTAAACATATATTATTATTGATTGCACTAAATTGAT
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTTCAGCTCTAAATAAAA
TGAAGGACTATCTAGGGTATTCAAAATGAATATCATGAACTCTCAATGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACCACCTCACATTCAAATGCCAAACATTCT
GCACAGGGAAGCTAGAGGTGGATAACACGTGTTGCAAGTATAAAAGCATCACTGGATTAAAG
GAGAATTGAGAGAAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAA
AA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 58

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKGLEETAACKGLGAKVHTFVVDCSNREDIYSSAKVKAEGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCCACCGCGTCCGGCGGACCGCGTGGGTGACTAGTTCTAGATCGCGAGCGGCCGCCGCCGCGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCCCTGAGAGGATGGTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCTGTTGATGCCTGGCCCGTGTGATGGGCTGTTCGCTCCCTATAACAGAAAGT
GTTTCCATGCCACCTAACGGAGACTCAGGACAGCCATTATTCTACCCCTTACATTGAAGC
TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTGGTCGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC
TTCCCAGCTCAGATAACAGCCAGAAGATGCCAGTAGTTCTGGCTACAGGGTGGGCCGGG
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGCCTATGTTGTCACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCGTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTACTGATGATACCCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTTATACAGTCAGTCAATTCACTAGTTCCAGATATTCTGAATATAAAAATA
ATGACTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCGTGAGAGAGGTGAAGATCAACCTGAACGGATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAACAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCCTTGAAATACTGGATAAAACTACTAGATGGCGACTAAC
AAGTGATCCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACGGAACCTGAGGATCAGCTTACTATGTGAAATTTCGACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACTATAGTTGAAAAGTACTTGCAGA
AGATACAGTACAGTCAGTTAACCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTACTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTCACCTATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA
TTCATTATGGAAAAGGATGGATCCTTATGTTGGAAAACTACCTCCAAAAGAGAACAT
CAGAGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTTCATCAATAAAATTATCCTTGAAACAAGTGAGC
TTTGTTTTGGGGGAGATGTTACTACAAAATTACATGAGTACATGAGTAAGAATTACA
TTATTAACCTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAATGA
AATTTAGGGCTTGAATAGGAAGTTTAATTCTCTAACAGAGTAAGTGAAGAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAGTCTTAGAACAAAAGAACATTCTTGAAATA
AAAATATTATATAAAAAGTAAAAAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGREL
SLVGPFPGLNMKSAYAGFLTvnKTynSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLRDRDFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNLPREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFELDKLLGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338,
348-352, 353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCCGGCTCCGAATGGCACATGTGGAATCCCAGTCTTGGCTACAACAT
TTTCCCTTCCTAACAAAGTCTAACAGCTGTTCAACAGCTAGTGATCAGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTGC
CCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCTGCTAACAGCTTCAAAAAACAGGAGCGACTCCACTGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTAGTCCTAACATTCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAATTTAAAAAGCAAGTATTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGAGGAGAAAGTATGTTAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACCACCAGGATGGGACCTGGTC
AGGCCAGCCTTTGCTCTCCCGAAATTATTTGGTCTGACCACTCTGCCTGTGTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGCTCTGCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
ATGCCTCAGTTCAGCACCTTCACTCTGAGAATCGTACTGGACCTCAACCAACTGACCGT
CCACCAAGGGACGGGGCGTCTATGTGGGGCATCAACCGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAACAGACAGGGCAGAAGAGGACAACAAGTCTCGTTACCG
CCCCTCATCGTGCAGCCCTGCAGCGAAGTGTCTCACCTCACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCTGTGGAGCCTCTACCAGGGGTCTGCA
AGCTGCTGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGACCATGTACGGGTGATTGTGCGCTCTGAGGGTGGAGA
TGGCAAGCTCTCATCGGCACGGCTGTGGATGGAAAGCAGGATTACTTCCCACCCCTGTCCA
GCCGGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGCTCTCCACTTGACAT
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGCTACTTCTCACTGTCCAGCCCGAGA
CCCCTGAGGCTGTGGCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGC
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGCTCCCTGCCCTGGCTGCACCCGGC
CGGGGTGGAATACCGCCTCTGCAGGCTGCTTACCTGGCCAAGCCTGGGACTCACTGGCCC
AGGCCTCAATATCACCAAGCCAGGACGATGACTCTTGCCTCTTCTCAAAAGGCAAG
CAGTATCACCAACCGCCGATGACTCTGCCCTGTGCTGCCCTCCATCCGGGCATCAACT
GCAGATCAAGGAGCGCTGCAGTCTGCTACAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGTCCCCATCGATGATAACTCTGTGGA
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCCGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTAGCTATTGGTGGAGATTAACTATAG
GCAACTTATTCTGGGAACAAAGGTGAAATGGGAGGTAAGAAGGGTTAATTGTG
ACTTAGCTTCTAGCTACTCCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCCAAACTTAAAGAAAAACTTAAGAAGGTACATGTCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNVNKLLIIDYSENRLLAGSL
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHYSVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFFIRAINLQIKERLQSCYQGEQN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328,
383-387, 384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGGGCTGAGTGC GGACTGGAGTGGAAACCCGGGCCCCCGCTAGAGAACACGCGATGACC
ACGTGGAGCCTCCGGCGAGGCCGGCCCCCACGCTGGACTCCTGCTGCTGGCTCTGGGCTTCCTGGTGC
CCG CAGGCTGGACTGGAGCACCCCTGGTCCCTGCGGCTCCGCCATCGACAGCTGGGCTGCAGGCCAAGGGCT
GGAACCTCATGCTGGAGGATTCCACCTCTGGATCTC GGGGCTCCATCCACTATTTGGTGTGCCAGGGAG
TACTGGAGGGACC CGCTGCTGAAGATGAAGGCTGTGGCTTAACACCCCTCACCACCTATGTCGTGGAACCT
GCATGAGCCAGAAAGAGGCAAATTGACTTCTCTGGGAACCTGGACCTGGAGGCTTCGTCTGATGGCCGAG
AGATCGGCTGTGGGTGATTCTCGTCCAGGCCCTACATCTGAGTGAAGATGGACCTCGGGGCTTGCCCAGC
TGGCTACTCCAAGACCCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTTCACCGAAGCAGTGGACCTTATT
TGACCACCTGATGTC CAGGGTGTGCCACTCCAGTACAAGCGTGGGGACCTATCATTGCCGTGCAGGTGGAGA
ATGAATATGGTCCATAATAAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATT
GTGGAACCTGCTCTGACTTCAGACAACAAGGATGGCTGAGCAAGGGGATTGTCCAGGGAGCTTGGCCACCAT
CAACTTGCACTGCAACACACAGCAGCTGCAGCTACTGACCACCTTCTTCAACGTCAGGGGACTCAGCCCAAGA
TGGTGTGGAGTACTGGACGGGTGGTTGACTCGTGGGGAGGCGCTCCATCAACCTCTACATGTCACGGAGGACCAACTT
TTGAAAACCGTGTCTGCCTATTGGACGGCGCTCCATCAACCTCTACATGTCACGGAGGACCAACTT
TGGCTTCATGAATGGAGGCCATGCACTTCATGACTACAAGTCAGATGTCACAGCTATGACTATGATGCTGTGC
TGACAGAAGCCGGCATTACACGCCAAGTACATGAAGCTCGAGACTTCTCGGCTCCATCTCAGGCATCCCT
CTCCCTCCCCCACCTGACCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTGTACCTGTCTGTG
GGACGCCCTCAAGTACCTGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATG
GGGGAAATGGACAGTCCTCGGGTACATTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCAC
GTGCATGATGGGGCAGGTGTTGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATTGC
TGTCCCCCTGATCCAGGGTTACACCGTGTGAGGATCTGGGGAGAATCGTGGGGAGTCAACTATGGGAGA
ATATTGATGACCAGCGCAAAGGCTTAATTGAAATCTCTATCTGAATGATTACCCCTGAAAAACTTCAGAATC
TATAGCTGGATATGAAGAAGAGCTTCTTCAGAGGTTGGCTGGACAAATGGNNTCCCTCCAGAACACC
CACATTACCTGCTTCTTGGTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTCTGAAGCTGGAGG
GCTGGGAGAAGGGGTTGTATTCAATGCCAGAACCTGGACGTTACTGGAACATTGGACCCAGAACAG
CTTACCTCCCAGGCTCTGGTGTGAGCAGCGGAATCAACCCAGGTACATCGTTTGAGGAGACGATGGGGGCC
TGCATTACAGTTACGGAAACCCCCCACCTGGCAGGAACCAAGTACATTAAGTGAGCGGTGGCACCCCTCTG
CTGGTCCAGTGGAGACTGCCCTCTTGACCTGAAGCCTGGTGTGCTGCCACCCCTCACTGCAA
AGCATCTCTTAAGTAGCAACCTCAGGGACTGGGGTACAGTCTGCCCTGTCTCAGCTCAAACCCCTAAGCC
TGCAGGGAAAGGTGGGATGGCTCTGGGCTGGCTTGTGATGATGGCTTCTACAGCCCTGCTTTGCG
AGGCTGTCGGCTGTCTAGGGTGGAGCAGCTAATCAGATGCCAGCCTTGCCCTCAGAAAAAGTGTG
AAACGTGCCCTTGCAACGGACGTCAAGCCCTGCCAGCATCTGCTGGACTCAGCGTGTCTTGCTGGTT
GGGAGGCTTGGCCACATCCCTATGGCCCCATTATCCCGAAATCTGGGTGTGTCACCAAGTGTAGAGGGTG
GGGAAGGGGTGTCTCACCTGAGCTGACTTTGTTCTTCTTACAACCTCTGAGCCTTGGGATTCTGGAA
GGAACCTGGCGTGAGAACATGTGACTTCCCTTCCCTCCACTCGCTGCTTCCACAGGGTGACAGGCTGG
GCTGGAGAAACAGAAATCCTCACCTCGCTTCCCAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGACA
TGTGAGTCTGGCAGAACGCCATGGCCATGTCTGCACATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTG
AGTCCTGGCAGAACGCCATGGCCATGTCTGCACATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTC
CTGGCAGAACCCATGGCCATGTCTGCACATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTC
CAGAACCCATGGCCATGTCTGCACATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTC
CCCCCACGCCGAACAGCAGGGGAGAGCAGCCCTCTCGAAGTGTGTCAGTCCGCAATTGAGCCTTGTTC
GGGGCCAGCCAAACACCTGGCTTGGCTCACTGTCTGAGTTGCAAGTAAAGCTATAACCTTGAATCAA

FIGURE 64

MTTWSLRRR PARTLGLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTYYVPWNLHEPERGKFDFSGNLDLEAFVLM
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLMMSRVVPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSNDNKDGLSKGIVQGVLAT
INLQSTHELQLLTTFLNVQGTQPKMVMEMWTGFDSWGGPHNILDssevlktvsaivdags
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP
LPPPPDLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNQSFYI
TSITSSGILSGHVHDRGQVFVNTVSIGFLDYKTTKIAVPLI QGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSPLKNFRIYSLDMKKSFFQRFGLDKWXSLPETPTLPAFFLGSLSIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544,
560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293,
309-315, 320-326, 366-372, 423-429, 425-431, 441-447, 503-509,
580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGCTAGCTAGGTGTAGGGTGGACGGTCCCAGGACC
CTGGTGAGGGTTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAGG
GGAGCAAAGCCGGCTCGGCCGAGGCCCGAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGCCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCTGCCTCGTCCCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTCGTTCTAGGGATAGGGTCACTGACCGTTCTCCTAGACGGGCCC
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTCGGTACCGCGGGTGTGGCCGAC
CGGCTTTGAAGATGCGATGGAGCGCCTCAACGCCATACAGTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATGCCCTCTGA
ATGAGGCAGCTAGCGAACCTGTTGGTCAACTGAGACAGGACCTACATCTGTGAGAG
TGGGAGATGGGGGGTCTCCCATCCTGGTTCGAAAACCTGAAATTCAAGAACCTC
AGATCCAGACTCCCTGCCGCAGTGGACTCCTGGTCAAGGTCTGCTGCCAAGATATATC
CATGGCTTATACAATGGGGCAACATCATTAGCATTAGCAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTCTCCGTGCACTGCTAGG
AGAAAAGATCTGCTTTCACCACAGATGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GAECTCTATACCACTGTAGATTTGGCCAGCTGACAACATGACCAAAATCTTACCCGTCTT
CGGAAGTATGAACCCATGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATT
CTGGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCATAAGAAGGGACGCTTCCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGACCCCACACCTAACGCTTTGCTCTCGAGATGTACAGCAAGT
TCCAGGAAGTTCTTGGGACCTTACCTCCCCGAGCCCCAACAGATGATGCTGGACCTGTG
ACTCTGCACCTGGTGGCATTACTGGCTTCAGACTGCTTGGCCCCGTGGGGCCAT
TCATTCAATCTGCCATGACCTTGAGGCTGTCAAGCAGGACATGGCTCATGTTGACC
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTATGGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTTGACGGGAAACTGGGTCAAACACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTGGGCTAACAGCAGTGACTCAAGGGCTGTTGAAGCCACCAATTCTG
GGGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTGCCTAACATGGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACCTGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCTCTACGTGCCAAGATTCCGCTGTTCCCTAGGGAGCCCTCAACAAAATTA
CATTGCTGGAACATAGAAGATGTACCTCTCAGCCCCAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGGACTTGAAAGGTAGGCCGGCATGGTGGCTCATGC
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCCAACATGGTAAACCCGTCTCCACTAAAAAATACAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC
AGGAGGCAGAGGTTGCACTGAGTGGAGGTTGACCAACTGCACCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAA

FIGURE 66

MAPKKLSSLRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAADVDSWFKVLLPKIYPWLYHNGGNIISIQVE
YGSYRACDFSYMRHLAGLFRAALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRVSATKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVPPLPPSPKMML
GPVTLHLVGHLIAFLDLLCPRGPIHSILPMTFEAVKQDHGFLYRTYMTHTEPEPTFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSAEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473,
550-554, 603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229,
227-233, 231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTGAAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC
ACCCACAATATGGCTTACATGTTGAAAAGCTTCTCATCAGTTACATATCCATTATTGTGT
TTATGGCTTATCTGCCCTACACTCTCTGGTTATTCAAGGATACTTGAAGGAATATT
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAACGATT
GCGTTCCCTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGTTAGTGAAAATAACTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGTGCCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCCCTGCTAACGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCCTGCCCTGGGTGTATTGCTAAAAAA
CCTTCGAGAGTTGTAATTAAAGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AAATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTAACAAAGTTAGTCATTCTAACGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACCTGGAT
TTAAAGTCCAATAACATTGCAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTTGTAAAATTATGGATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA
AAAACTTGGAGTCACTTATTCTCTAACACAAGCTCGAACCTTACAGTGGCAGTATT
AGTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCAGGCTTGTG
TGGAAGATCACCTTTGATAACCTGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGGATTAAACTAAGATAATATATGCACAGTGATGTGAGGAAC
AACTTCCTAGATTGCAAGTGCTACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGAGGTTAAAGTCATTCAAATCATTCCCCCTTTGGGG
AAAGGGAAAGGAAAATTATAACTAAATCTTGGTTCTTTAAATGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDI PDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLS
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMNTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPA W VYLLKNLRELYLIGNLNSENNKMIGLES LRELRLKILHVKSNLTKVPSN
ITDVAPHLT KLV HNDGT KLLVLNSLKKMMNVAELELQNCELERI P HAIFSLSNLQELDLKS
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTI PPSITHVKNLESLYFSNNKLES LPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITS LP
EKVGQLSQLTQLELKGNCLDR LPAQLGQC RMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCGTCCGGCCTCTCTGGACTTGCATTCCATTCTTTCATGACAAACTGACTTTTTATTC
TTTTTTCCATCTCTGGCCAGCTGGATCCTAGGCCCTGGGAAGACATTGTGTTTACACACATAAGG
ATCTGTGTTGGGTTCTCTCCCTCCCCTGACATTGGCATTGCTTAGTGGTTGTGGGGAGGGAGACCACG
TGGGCTCAGTGCTTGCTGCACTTATGCCTAGGTACATCGAAGTCTTGACCTCCATACAGTGATTATGCC
TGTCACTGCTGGTGGTATCCTGGCGCCCTGCTCTGCTGATAGTTGTCGTGCTCTGCTTACTTCAAATAC
ACAACCGCCTAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAAACCCAGACAAGGTGTGGTGG
GCCAAGAAGCAGGCCAAACATTGCCACGGAGTCTTGCTGCTGCCCTGCAGTGCTGTGAAGGATATAGAAT
GTGTGCCAGTTGATTCCCTGCCACCTGCTGTCGACATAATGAGGGCCTCTGAGTTAGGAAAGGCTCCC
TTCTCAAAGCAGGCCCTGAAAGACTTCATGTCATGAGCCCTGCTGGTGTGAGTGTGAGGACAGAAGA
AAGGCACAGCTCCCCATCAGTTCATGAAAATAACTCAGTGCTGCTGGGAAACCAGCTGCTGGAGATCCCTAC
AGAGGCTTCACTGGGGCAACCCCTCAGGAAGGAGTTGGGAGAGAACCCCTACTGTGGGAATGCTGA
TAAACCAAGTCACACAGCTGCTCTATTCTCACAAATCTACCCCTGCGTGGCTGGAACTGACGTTCCCTGGA
GGTGTCCAGAAAGCTGATGTAACACAGAGCCTATAAAAGCTGTCGGCTCTAAGGCTGCCAGCGCTTGCAA
**AATGGAGCTTGTAAAGAAGGCTCATGCCATTGACCCCTCTAATTCTCTCTGTTGGCGAGCTGACAATGGCG
AGGCTGAAGGCAATGCAAGCTGACAGTCAGTCTAGGGGTGCCAATATGGCAGAGAACCCCAAAGCCATGATC
CTGCAACTCAATCCAGTGAGAACTGCAACCTGGACAATAGAAAGACCAAGAAAACAAAAGCATCAGAATTATCTT
TTCCTATGTCCAGCTTGATCCAGATGGAAGCTGTAAGTGAACATTAAGTCTTGACGGAACCTCCAGCA
ATGGGCTCTGCTAGGGCAAGTCTGAGTAAAACGACTATGTTCTGTATTGAAATCATCATCCAGTACATTG
ACGTTTCAAATAGTTACTGACTCAGCAAGAATTCAAAGAACTGTCTTGTCTTACTACTTCTCTCTCAA
CATCTCTATTCAAACGTGGCGTTACCTGGATACCTGGAAAGGATCCTCACAGCCCCAATTACCCAAAGC
CGCATCCTGAGCTGGCTATTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAACTTCAA
GAGATTTCCTAGAAAATAGACAAACAGTCAAATTGATTCTTGCCATCTATGATGGCCCTCCACCAACTC
TGGCCTGATTGGACAAGTCTGGCGTGTGACTCCCACCTTCGAATCGTCATCAAACCTCTGACTGCTGT
TGTCTACAGATTATGCCAATTCTACCGGGATTCTGCTTCTACACCTCAATTATGCAAGAAAACATCAAC
ACTACATCTTAACCTGCTCTCTGACAGGATGAGAGTTATTATAAGCAAATCTACCTAGAGGCTTTAACTC
TAATGGGATAACTGCAACTAAAGACCAACTTGCAAGACAAAATTATCAAATGTTGTGAAATTCTGTCC
CTCTTAATGGATGTTGACAATCAGAAAGGTAGAAGATCAGTCATTAACACCAATAATCACCTTTCT
GCATCCTCAACTTCTGAACTGATCACCCCTCAGAAAACAACCTCAGATTATGTAAGTGTGAAATGGGACATAA
TTCTACAGTGGAGATAATACATAACAGAAGATGATGTAATACAAAGTCAAATGCACTGGGAAATATAACA
CCAGCATGGCTCTTTGAATCCAATTCTGAAAAGACTACTTGAATCAGTCATTAACACCAATTATGTTGAAAC
CAAACCTTTGTCAGTTAGTCTGCACACCTCAGATCAAATTGGTGGTTCTGATACCTGTAGAGC
CTCTCCCACCTCTGACTTGCATCTAACCTACGACCTAATCAAGAGTGGATGTGAGATGAAACCTGTA
AGGTGTATCCCTTATTGGACACTATGGAGATTCCAGTTAATGCCCTTAAATTCTGAGAAGTATGAGCTCT
GTGTATCTGCAGTGTAAAGTTGATATGTGATAGCAGTGACCCACAGTCGCTGCAATCAAGTTGTCTC
CAGAAGCAAACGAGACATTCTTCATATAAATGGAAAACAGATTCCATCATAGGACCCATTGCTCTGAAAAGGG
ATCGAAGTGCAGTGGCAATTCAAGGATTTCAGCATGAAACACATGCGGAAGAAACTCCAAACCCAGCCTTCAAC
AGTGTGCATCTGTTCTCATGGTTAGCTCTGAATGTGGTGAAGTGTAGCGACAATCACAGTGAGGCATT
TGTAAATCAACGGGCAGACTACAAATACCAGAAGCTGCAAGACTATTAACTAACAGGTCAAACCTTAAGTGAGA
CATGTTCTCCAGGATGCCAAGGAAATGCTACCTCGTGGCTACACATATTGAATAAATGAGGAAGGGCCTG
AAAGTGACACACAGGCCTGCATGTAAAAAA**

FIGURE 70

MELVRRLMPLTLIILSCLAEALTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLGVCSKNDYVPVFESSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYWKTDIIGPIRLKRDRSASGNQGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375,
379-383, 408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCTGCGCCG
GGACATGCGGCCCGAGGAGCTCCCAGGCTCGCGTCCGTTGCTGCTGTTGCTGC
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCACCGCCTCGACCCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGCTGGTTGACCAGGCCAAGTCGGCATCTCATCCACTG
GGGAGTGTTCCTCGCCAGCTCGTAGCGAGTGGTCTGGTGGTATTGGCAAAAGGAAA
AGATAACCGAAGTATGTGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT
TTTGGACCACTATTACAGCAAATTTTAATGCCAACAGTGGGCAGATATTTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACCTCCAAACATCATGAAGGCTTACCTTGTGGGGT
CAGAATATTCTGGAACCTGGAATGCCATAGATGAGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGAACAGAACTGACCTGCCGTTGGACTGTACTATTCCCTTTGA
ATGGTTTCATCCGCTTCTGAGGATGAATCCAGTTCAAGCGGAATTCCAG
TTCTAACAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG
TCGGATGGTACGGAGGAGCACGGATCAAACTGGAACAGCACAGGCTTGGCCTGGT
ATATAATGAAAGCCCAGTCGGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATAACCTGCAGTGATCGTTATAACCCAGGACATCTTGCCA
CATAAATGGAAAAGTGCATGACAATAGACAAACTGCTCTGGGCTATAGGAGGGAAAGCTGG
AACTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTCGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGTCTGGCTAAAGTCAATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTCCTAAATGGCCACATCAGGACAGCTGTCCTGCCAT
CCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC
GATTTCTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC
CGTGTAAATGGGCTGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAAACTGGATAAGAAAATTATTGGCAGTTGCCCTTCCCTTTCCACTA
AATTTCCTTAAATTACCCATGTAACCATTAACTCTCCAGTGCACCTTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTATGTTGAAGCCATATCCCCCATG
ATTATAATGTTATGCATCACTTAATATGGGATATTTCCTGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAATCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG
AAATACTGTAGGCAATAGTAACAGTGGTATTGTATATGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAAAATAATGGGCACCTGTATAGGGACCTTACCAAGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTCAATTATAAACTAACATAAGTGTACTGTAACCTTACAAACGTTTAATT
TTTAAACCTTTGGCTTTGTAATAACACTTAGCTAAACATAAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFLPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFQAKFGIFIHWG
VFSVPSFGSEFWWYWQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSPKKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNW
SLEQNGIMVELPQLTIHQMPCKWGWLALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280,
315-319, 375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT
TCCAGAAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACG**A**TGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCATCTGGACCACGAGGCTCTGGCCAAGGCTCTTGCAGAAGAGCT
TTCCATCCAGGTGTATGCAGAATTATGGGGATCACCCCTGTGAGCAAAAAGGCGAACCAAGC
AGCTGAATTCACAGAAGCTAAGGAGGCCGTAGGCTGCTGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGCAGCTATGGCTGGGTTGGAGA
TGGATTCGTGGTCATCTCTAGGATTAGCCAAACCCAAAGTGTGGAAAAATGGGGTGGTG
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACACTCATCTGAT
ACTTGGACTAACCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATTCAACACTCA
AACTGCAACACAAACAGAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTT
ACTCTACAATAACCTGCCCTACTACTACTCCCTCGCTCCAGCTTCACTTCTATTCCACGG
AGAAAAAAATTGATTGTCACAGAAGTTTATGGAAACTAGCACCAGTCTACAGAAAC
TGAACCATTGTTGAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTG
CCACGGCTCTGCTAGTGCTTGCTCTCCTCTTGGTGCAGCTGGCTTGGATTTC
TATGTCAAAAGGTATGTGAAGGCCCTCCCTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAGCAAAACTACCGTGCATGCC
CCTGAAGTT**AG**ATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCAGCTGGGAAATCAAAAGGCCAAGAACCAAGAACAGAAAGTCCACCC
GGTTCTTAACCTGAAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCAACAAAGAGAATGC
CCTTCTCCTTATTGTAACCTGCTGGATCCTATCCTCCTACCTCAAAGCTCCACGGCC
TTCTAGCCTGGCTATGCTTAATAATATCCCCTGGAGAAAGGAGTTTGCAAAGTGCAA
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCAGTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAAACACGTATCCACCTGACATGTCCTCTGAGCCCCGTA
AGAGCAAAAGAATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACCTGAG
ACCTAATCTCTGTAAGCTAAAATAAGAAATAGAACAAAGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAACACAGACAGGGTCAAAGTGTGTTCTGAAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATAATTCTCT
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTCTATTCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTCT
GTTTGATATTCTAGCTTATCTACTTCCAAACTAATTCTATTCTGAGACTAATCTT
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTATAACACACTAACAG
TACATTGTTACCTCTATATACCAAAGCACATTAAAAGTGCCATTAAACAAATGTATCACTA
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNSPKCGKNGVGVLIWKPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVSPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASFNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDRNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTGGCACCTCTAATTGCTCTCGTGTATCGGTGCCCGACTTCACGATGG
CTCGCCAACCTTACTACCTTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGA
ACTGCCGCCGCTCTGCCACGGCTGCCACCCAACGCGAAGACGGTAACCGTGTACTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAAGCAACATTTCATGTTAGTAAAGTGGCCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCATGATAAA
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTGGATTGGAGTTGCCAA
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGGAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGTAC
AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCGTATGCTGACCTCC
GGAGGCAATGCCGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACACAGTCAGA
TGGGAAAACAAGAAGGATAAAGATCCTCACTTGGCAGTGCTCCTCTGTCAATT
CCAGGCTCTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGAATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCAACTGTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTCCCTCAAGCTGGTCAGTGTGTTACTGCTTATC
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTTAG
TTGACCTGCACAGCTGGTAGACCTAGATTAAACCTAACGTAAGATGCTGGGTATAGAA
CGCTAACGAAATTCCCCAAGGACTCTGCTCCTAACGCCCTGGCTTGTGTTATGGTC
TTCATTAAGTATAAGCTAACCTTGTGCTAGTCCTAACGGAGAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCCCTATTGTGGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGCTGGTAGGACTGGAGGAGAAATCCCTGGACTTCAC
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAFLLVRKLPPCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMF SKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNI PEEQPVASTPTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGACGTTGCCCTG
GGGCCAGCCTGGCCGGTCACCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCC
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTACAACGGCTTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGGAGACCCCTGTTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGGCGTGTGCGTGTCAAATGGTGGAAAGCT
GTCGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATGGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTGCACCTGCGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTCGGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTCCTTACAGTCCCCCA
ACGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCCGTG
GTGGCCTCCTTGAGCAGCTCTCCGGGCCTGGAGGAGGGCCTGGACTGGTGCAACCGGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCCGTGGCC
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCGCCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCCGTAGAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC
AGCTTTGCCGCTGGAAGTTCCATGGCCTGGACCGCTGCAGCCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCGTGGTTCACCCGATCTAACTGTGGCCCCAGAGCCTGGGT
CCGAAGCTTGGCTTCCCCGACCCGAGAGCCGCTTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGGCCCTCCCTGCCGATTCCCTACTGGCTGTGATTATTGAGTGGTT
CGTTTCCCTTGTGGGTGGAGCCATTTAACTGTTTATACTTCTCAATTAAATTCT
TTAAACATTTTTACTATTTTGAAAGCAAACAGAACCCATGCCCTTGTGCTCCTG
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGGCATTTGCAGGTTGGCTGGCTTCTG
GAGGGTTCCCCGCCATCCAGGCTGGCTCCCTCCCTTAAGGAGGTTGGCTGGCAGAGTGGC
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGGATGGTGGGCACAGTTCTCCCTGCC
CAGCCTGGGGAAAGAAGAGGGCCTGGGGCCTCCGGAGCTGGCTTGGCCTCTCCTGCC
CACCTCTACTCTGTGAAGCCGCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAAACTCCCTCCCCGTTCCCT
TCCCTCTCGGTTCAAAGAATCTGTTGTCATTGTTCTCCTGTTCCCTGTGTTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGCTATGACTGCCCTCCGCCAA
AAA
A

FIGURE 78

MGLLLLVPLLLPGSYGLPFYNGFYYNSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFVQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEELDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGYPR
HRRLLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**A****T**GATGTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGCGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA
CTTCCAGTACGACCATGAGGCTTCCTGGACGGGAAGTGGCCAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGCTGGGGCGGATCGTGACCGCATGGACCGCGCGGGGAC
GGCGACGGCTGGGTGTCGCTGGCGAGCTCGCGGTGGATCGCGCACACGCAGCAGCGCA
CATACGGACTCGGTGAGCGCGGCTGGACACGTACGACACGGACCGCGACGGCGTGTGG
GTTGGGAGGAGCTGCGAACGCCACCTATGCCACTACGCCCGGTGAAGAATTGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGGACGAGCGCGTGGCTCCGGTGGC
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCCTGCACCCCGAGG
AGTTCCCTCACATGCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGGGATCTGTACTCAGCCGAGCCTGGGAGGA
GGAGCCGGGTGGGTGCAGACGGAGACGCAGCAGTTCCGGACTTCCGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGTGCTGCCCCCTGCCAGGACCAGCCC
CTGGTGAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCCTGGTAATTGAAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCACGATGAGCTG**T****A**GCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACGGAGGAGGGGGCCCTGTGGCTGGCCCTCCCTGTCCAGGCCCCGAGGAG
GCAGATGCAGTCCCAGGCATCCTCCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC
TGTCCCTGTACACCCCCAACCCAGGGAGGGCTGTCAAGTCCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACACATAGACTGAAACTCCCCT
GGCCCCAGCCCTCTCCTGCCCTGGCCTGGACACCTCCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDRDGRVGWEELRNATYGHYAPGEFFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGHLDGSEVGHVLPPAQDQPLVEANLLHESDTDKGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GC GGCGGGCGGGGTGCGAGGGATCCCTGACGCCCTGTCCCTGTTCTTGTCGCTCCCAG
CCTGTCTGTCGTTGGCGCCCCGCCCTCCCCCGGGTGCAGGGGTTGCACACCGATCCTG
GGCTTCGCTCGATTGCGCCGAGGGCGCTCCCAGACCTAGAGGGGCGCTGCCCTGGAGCAG
CGGGTCGTCTGTGTCCTCTCCTCGGCCGCCGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACCGCGGGGCCTCCGCACCCCTGGCCTGCCGATTCTCCCTCTCTCCAG
GTGTGAGCAGCCTATCAGTCACC**ATGT**CCGCAGCCTGGATCCGGCTCGGCCCTGGTGTG
TGTCTGCTGCTGTCGCCCCGGCCGGCAGCGAGGGAGCCGCTCCATTGCTATCACATG
TTTACCAAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC
CTCTTGAGGAATTCTCTGTATGGAACATAGTATATGCTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTAGCCTACC
TGGTCGAGAAAACATTCCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTTCTTCACAGTAACTAAGGAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAACAGACTAAAGAAAACACCCGAGAAGAAAACCTGG
CAATAAAGATTGTAACAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGGCAGC
GCCGATTTAATTACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGGAAATTGGAACA
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATT**T**ACTTGAA
AAACTTACATCAGCCAAGATGTTGTTGCCATAAAGGAAGTÄGGTTAGAGGGGTA
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGATCCCAAAGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACCTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTTACACATGCCCAACTGGTTGGCACCCACAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTCACTCATGAACAAATGATGTGCAAGACCTGTTATAACT
CAGTGAACATTGCCCTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCCCTC
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA
AAGAGAATGTCTTAGCTGTCACTGTTAGAAATGTGTTGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTGTTGGTGTGGCTGGCACCTCTGGATGACCTG
AAAGATATGGCTCTAAACCGAAGGAGTCTCACGCTTCTCACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCACTCAGAGGCATTGTTAGAGATTCTTAGAATCCCAGCAAT
AATGGTAACATTGACAACTGAAAGAAAAAGTACAAGGGATCCAGTGTAAATTGTATT
CTCATAATACTGAAATGTTAGCATACTAGAATCAGATAAAAATTAAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTTCTAGAAAATCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCAACCATGCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAA

FIGURE 82

MSAAWI PALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCLEEF SVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKT FEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381,
420-424, 425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGGCTCCGCACCCGGGCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC
GGCGGCCTCCGGGGAGCGAGCAGATCCAGTCCGGCCCGAGCGCAACTCGGTCCAGTCG
GGCGGGCGCTCGGGCGCAGAGCGGAGATGCAGCGGCTTGGGCCACCTGCTGTGCCTGC
TGCTGGCGGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCGGCCGGCTCTCAGTACCCGAGGAGGCCACCCCTCAATGAGATGTTCCCGCA
GGTTGAGGAAGTGAAGGAGACACGAGCACAAATTGCGCAGCGCGTGGAAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCCAGCTAT
CACAATGAGACCAACACAGACAGAACAGGTTGAAATAATACCATGTGCACCGAGAAAT
TCACAAGATAACCAACACCAGACTGGACAAATGGTCTTTAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTAAGTGCAGTTGCCAGCTTCCAGTACACCTGCCAGGCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCCTCCAGAGAGGGCTGCTGTTCCCTGTGTCACACCCCTGCCGTGGAGGGCGA
GCTTGCATGACCCGCCAGCCGGCTTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTGGACCGATGCCCTGTGCCAGTGGCTCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTGTGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTGTGAGCTTACATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGGAGCCTGACTGAAGAGATGGCCTGGGGAGCCTGCCGGCTGCCGCT
GCACTGCTGGGAGGGAAAGAGATTAGATCTGGACCAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCAGGTGTGCTTCTGGCTGGGCTGACAGCAGTGGTAGTGTGCAATTGTT
TCTTCTCCAGTAAGTTCCCTCTGGCTGACAGCAGTGGTAGTGTGCAATTGTT
TCCCCCAGGCTGTTCTCAGGCTCACAGTCTGGCTTGGAGAGTCAGGCAGGGTTAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACCAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAATGTGG
AGTCTCCCTCTGATTGGTTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAACATCAA
CCTGGAAAAATGCAACAAATGAATTTCACGCAAGTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTCAGATGAAATGTTCTGTCACCCCTGCATTACATGTGTTATT
AGCAGTGTGCTCAGCTCACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGAGGGGTCTTCTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGCAGTT
CTGGTTGTGACTCTAAGCTCAGTGTCTCTCCACTACCCACACCAGCCTTGGTGC
AAAGTGTCCCCAAAGGAAGGAGAATGGGATTGGTCTTGAGGCATGCACATCTGG
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGT
AGTGTGGGCAGCCGCTCTCTAATGAAGACAATGATATTGACACTGTC
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATACAGGTT
GTACTTAGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAA
TGAAGACAATTATCAACCAACAGTGGAGAAATCAAACCGAGCAGGGCTGTG
GTAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATGTT
TGGACTGTTGCCACCATGTATTGACAGTTCTAAAGTTAAAGTTGCACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGATAAACATAAGTTGCATTAG
ATAAAATCACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECI IDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCQAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPACASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCT
GAAGATAACAATAATTTCAGCCCCATCCACTCTCCTTCCCTCCAAACACACATGTGCATGTACACACACACATA
CACACACATACACCTTCCCTCCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTATAGAAAAGGA
CACTAAAGCCTTAAGGCAGGGCCTGGCATTACCTCTGCAGCTCTTGGCTTGAGTCAGGAAACATGGGA
GGGGCCAGGCACGGTGAACACACCTGTAATCCCAGCATTTGGAGACCGAGGTGAGCAGATCACTTGAGGTC
AGGAGTTGAGACAGCAGCTGGCCAACATGGAGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGAGT
GGTGGCAGGTGCTGTAATCCCAGCTACTCAGGTGGCTGAGGCCAGGAGAATCGCTGAACTCCAGGAGGCGGAGG
ATGCCAGTCAGCTGACGTCACCTCCAGCCTGGCTGACAGAATGAGACTCTGTCTCAAACAAACAAACA
CGGGAGGAGGGTAGATACTGCTTCTGCAACCTCTTAACCTGATCCTCTTCCAGGGCTGCCCTGTA
TGGGGCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAGGAAGAGAAGGCATATTGAGGAGGGCAAGAA
GTGACGCCGGTGTAGAATGACTGCCCTGGGAGGGTGGTCTTGGGCCCTGGCAGGGTTGCTGACCCCTAACCT
TGCAAAACACAAAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCCCTGCCCTGAGCTCCACCATGAGGCT
TCTCGGCCCTACTTGCTAGCTTGGTGGCTGGACTGCCACTGTCGCCCCGTGGTACCCCTGGCATGTT
CCTGCCCTCTCAGTGTGCCCTGCCAGATCCGGCCCTGGTACAGCCCCGCTGTCTACCGCGAGGCTACCAACT
GTGGACTGCAATGACCTATTCCCTGACGGCAGTCCCCCGGCACTCCCCCGCAGGACACAGACCTGCTCCGTCA
GAGCAACAGCATTGTCGTGGACCAGAGTGAACGGTGGCTACCTGGCCAATCTCACAGAGCTGGACCTGCTCC
AGAACAGCTTTTGGATGCCGAGACTGTGATTTCCATGCCCTGCCAGCTGCTGAGCCTGACACCTAGAGGAG
AACCAAGCTGACCCGGCTGGAGGACCACAGCTTGACGGGCTGGCAGGCTACAGGAACCTATCTAACCAACAA
CCAGCTCTACCGCATGCCCTCAGGGCTTTCTGGCCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACC
TCCTGAGGGCATTGACAGCCGCTGGTTGAAATGCTGCCAACCTGGAGATACTCATGATTGGCGGCAACAAG
GTAGATGCCATCTGGACATGAACCTCCGGCCCTGGCCAACCTGCGTAGCCTGGTCTAGCAGGATGAACCT
GCCGGAGATCTCCGACTATGCCCTGGAGGGCTGCAAGGCTGGAGAGGCTCTCCTCTATGACAACCAGCTGG
CCCGGGTGCCAGGGCCACTGGAACAGGTGCCGGCTCAAGTCTCTAGACCTCAACAAGAACCCGCTCCAG
CGGGTAGGGCCGGGGACTTGGCAACATGCTGACCTTAAGGAGCTGGACTGAAACAACATGGAGGAGCTGGT
CTCCATCGACAAGTTGCCCTGGTGAACCTCCCCGAGCTGACCTGGAGGACTCACAATAACCCACGGCTGT
CCTCATCCACCCCCCGCCTTCCACCCCTGCCAGATGGAGACCCCTATGCTCAACAACACGCTCTCAGT
GCCCTGCAACCAGCAGACGGTGGACTCCCTGCCAACCTGCAAGGAGGTAGGTCTCCAGGGCAACCCATCCGCTG
TGACTGTGTCATCCGCTGGCCAATGCCACGGCACCCGTGTCCGCTTCATGAGGGCAATTCCACCTGTGTG
CGGAGCCTCCGACCTCCAGCGCTCCGGTCCGTGAGGTGCCCTCCGGAGATGACGGACCACTGTTGCC
CTCATCTCCCCACGAGCTTCCCCCAAGCCTCCAGGTAGCAGTGGAGAGAGCATGGTGTGCTGATTGCCGGC
ACTGGCCAACCGAACCCGAGATCTACTGGTCACTCCAGCTGGCTTCTGACTGACACCTGCCATGAGGCA
GGAGGTACCGGGTGTACCCGAGGGGACCTGGAGCTGCGGAGGGTACAGCAGAAGAGGAGGGCTATACACC
TGTGTGGGCCAGAACCTGGGGGCTGACACTAACAGCGTTAGTGTGGTTGTGGCCGTGCTCTCCTCAGCC
AGGCAGGGACGAAGGACAGGGCTGGAGCTCCGGGTGAGGAGACCCACCCCTATCACATCTGCTATCTGGG
TCACCCCACCCAAACACAGTGTCCACCAACCTCACCTGGTCACTGCCCTCCCTGGGGCAGGGGCCACA
GCTCTGGCCCGCCTGCCCTGGGAACCCACAGCTACAACATTACCGCTCTTCAGGCCACGGAGTACTGGC
CTGCCCTGCAAGTGGCTTGTGATGCCACACCCAGTTGGCTGTATGGGCCAGGACAAAGAGGCCACTT
CTTGCCACAGAGCCTTAGGGGATGTCCTGGCTCATTGCCATCTGGCTCTGCTGCTCTCTGGCAGCT
GGGCTAGGGCCACCTGGCACAGGCCAACCCAGGAAGGGTGTGGGAGGCGGCCCTCCCTCCAGCCTG
GGCTTCTGGGGCTGGAGTGGCCCTTCTGTCCGGGTTGTGCTGCTCCCTCGCTGCCCTGGAATCCAGGGA
GGAAGCTGCCAGATCCCTCAGAAGGGAGAGACACTGGCCACATTGTCTCAAATCTTGTGAAGCTCAGGCTGT
TCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACCAAAAGAGAACAGCTGGCCAGATGCCCTGCCAGG
AAAGGGACATGGACCCACGTGCTTGAGGGCTGGCAGCTGGCCAAGACAGATGGGCTTGTGGCCCTGGGGT
GCTTCTGCAAGCCTGAAAAGTTGCCCTTACCTCTTAGGGTACCTCTGCTGCCATTCTGAGAACATCTCAA
GGAACAGGGAGGGACTTGGCTAGAGCCTCCCTGCCCTCCCTACCTCTGCTGCCAGGGCTCTGGGCCCTGG
TGGCTGCCCCACTCTGTGTCCCCGGCTGCACCCCTTCTCTTCTGTACAGTCTCAGTTGCT
TCTTGTGCCCTCTGGCAAGGGCTGAAGGAGGCCACTCCATCTCACCTGGGGGCTGCCCTCAATGTGGAGT
GACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAACGCCCTATCTCAGCAGCCTGGGCCGG
CATTCGAAGCTGACTTTCTATAGGAATTGTACCTTGAGGAAATGTGTACCTCCCCAACCCGATTC
ACTCTTTCTCCTGTTGTAAAAAATAAAAATAAAACAATAAAAAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTEDLSQNSFSDARCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSVLVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLQPQMETLMLNNNALSHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGADTKTVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLA AHLGTGQPRKGVGGRRLPLPPAWAFWGWSAPS VRVV
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCCTGTTGAGAAGGTGAAGAACGGACCCATGTGGAGGAGGGGACATTGTGTACCGCC
TCTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCAC
AACATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGGCTGACGGGCTACCGCACCTACCGCTGTGCCA
CCCCCTGCCACACTCTCAAGATCCTGGCTCCTTACATCAGCCTAGTCATCTACGCCCTACATCTGCA
TGTACACACTGTGGATGCTACGGCCTCCCTCAAGAAGTACTCGTTGAGTCATCGTGAGGAGAGCAGC
TACAGCGACATCCCCGAGCTCAAGAACGACTTCGCCCTCATGCTGCACCTCATGACCAATACGACCCGCTCTA
CTCCAAGCGCTCAGCGCTCTCTGAGGTGAGTGAGAACACAAGCTGCCAGCTGAACCTCAACAAACGAGT
GGACGCTGGACAAGCTCCGGCAGCGGCTACCAAGAACAGCGCAGGACAAGCTGGAGCTGCACCTGTCATGCTC
AGTGGCATCCCTGACACTGTGTTGACCTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGAC
CATCCCGCCAGCATTGCCAGCTCACGGGCTCAAGAGCTGCTGAGCTACACACAGCGGCCAGATTGAAG
GCCCTGCCCTGGCTTCCCTGCCAGAACCTGCCAGGCCCTGACATCAAGTTCACCGACATCAAGGAGATCCCC
CTGTGGATCTATAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGCAACCTGAGCGCGAGAACAAACGCTA
CATCGTCATCGACGGGCTGCCAGCTCAAACGCTCAAGGTGCTGCGCTCAAGAGCAACCTAAGCAAGCTGC
CACAGGGTGTACAGATGTGGCGTGCACCTGAGAAGCTGTCCATCAACATGAGGGCACCAAGCTCATCGTC
CTCAACAGCCTCAAGAACGATGGCGAACCTGACTGAGCTGGAGCTGATCGCTGCGACCTGGAGCGCATCCCCA
CTCCATCTTCAGCCTCCACAACTGCAAGGAGATTGACCTCAAGGACAACCTCAAGACCATCGAGGAGATCA
TCAGCTTCAGCACCTGCACCGCCTCACCTGCCTTAAGCTGTGGTACAACACATCGCTACATCCCCATCCAG
ATCGGCAACCTCACCAACCTGGAGCGCCTTACCTGAACCGCAACAAGATCGAGAACGATCCCCACCCAGCTCTT
CTACTGCCGCAAGCTGCGTACCTGGACCTCAGCCACAACAAACCTGACCTTCCCTGCCGACATGCCCTCC
TGCAGAACCTCCAGAACCTAGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTCCAGTGGCGG
AAGCTGGGGCCCTGCACCTGGCAACAAACGTGCTGCAGTCAGTGCCTCCAGGGTGGCGAGCTGACCAACCT
GACGCAGATCGAGCTGCCAGGGCAACCGGCTGGAGTGCCTGCTGTGGAGCTGGCGAGTGCCACTGCTCAAGC
GCAGCGGCTTGGTGGAGGAGGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGTGTGGAGGGCT
GACAAGGAGCAGGCTTGAGCGAGGCCAGCACAGCAAGCAGCAGCAGGACCGCTGCCAGTCCCTCAGGCCCGG
AGGGCAGGCCAGCTAGCTTCCCAGAACACTCCGGACAGCCAGAGCAGCCTCGCCGCTGGCAGGAGCTGGGCC
GCTTGTGAGTCAGGCCAGAGCAGAGGAGACAGTATCTGTGGGCTGGCCCTTTCTCCCTCTGAGACTCACGTC
CCCCAGGGCAAGTGTGTTGGAGGAGAGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCCCTCCG
GAGGCCAGCTCTGCCAGGGCTGAGCTGCCACCCAGAGGTCTGGGACCTCAGTTAGTTCTGGTATTAT
TTTCTCCATCTCCACCTCCATCCAGATAACTTATACATTCCAAAGAAAGTTCAGCCCAGATGGAAGGTG
TTCAGGGAAAGGTGGCTGCCCTTCCCTGTCCATTAGCGATGCCGGCATTAAACACCCACCTGG
ACTTCAGCAGAGTGGTCCGGCGAACCCAGCCATGGGACGGTCACCCAGCAGTGCCTGCTCTCAGTTTGCGAGTT
CGGTCCACGGGAGAGCAGGCCAGCTGGAAAGGCCAGGCCAGTGGAGCTTGCCTCTCAGTTTGCGAGTT
TTAGTTTTGTTTTTTTTAATCAAAAAACAATTTTTTAAAAAAAGCTTAAAGACACTAACGCCAGTGGAGTCTCAGGGCAGG
GGTATTAAAAAGAAAAAAACTTAAAAAAAGACACTAACGCCAGTGGAGTCTCAGGGCAGGGTGCAGGGT
TCTTCCGGATCTGGTGTGACCTTGGTCAGGAGTTCTATTGTTCTGGGAGGGAGTTTTGTTGTT
TTGGTTTTGGTCTTGTCTTCTCCATGTGCTTGGCAGGCACTATTCTGTGGCTGCGC
CAGAGGGAAATGTTCTGGAGCTGCCAAGGAGGGAGACTCGGGTGGTAATCCCGGATGAACGGTGTCC
TTCGCACCTCCCTCTCGTGCCTGCCCTGCCCTCCACGACAGTGTAAAGGAGCCAAGAGGGAGCCACTTCG
CCAGACTTGTCTCCACCTCTCGGCCATGGGTGTCCAGTGCCACCGCTGCCCTCCGCTGCTCCCATCAG
CCCTGTCGCCACCTGGTCTCATGAAGAGCAGACACTTAGAGGCTGGTGGGAATGGGAGGTGCCCTGG
AGGGCAGGCCAGTGGTCCAGGCCGGTCCCGTCCGGAGTGCACACAGCCAGTCCGCCACCTGG
GCTGGAAAGCCAACCTGCTTAAAGTCACTGGGTCCTTACCTAGAAGGGTCCCCGCTTAGATCAATCAGTGG
ACACTAAGGCACGTTAGAGTCTTGTCTTAATGATTATGTCATCCATCCGTCTGTCCTGCTCCATTGTT
GCCTCGTGTCAATTGATATAACCTCAGAAATAATGCACACTAGCCTCTGACAACCATGAAGCAAAATCCGTT
ACATGTGGCTGACTTGTAGACTCGGTACAGTATCAAATAACAGAAAAAAATCCGTT

FIGURE 88

MRQTIIKVIKFILIICYTVYYVHNIFDVDCVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSKR
RFAVFLSEVSENKLRQLNLNEWTLDKLQRQLTKNAQDKLELHLFMLSGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFRLRENLRALHIKFDTIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHLCNNVLQSLPSRVGELETNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436,
491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGTCAATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTCCATTCTACATTTCTCAGAGTCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCAACTTGCAGGGGT
TGCCTTGGGTGATTCCCTGGATCTCCCTGTTGATTGGTGCCTCCTGGGACCTTACCTGT
ACAGCATGTCTCTCTCGAACGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGGCCACCTAGTTGTCTTCAGCGC
CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGCCCATCAGAAAGAA
GCTCAAAATTATCCCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGCCTG
GGTGCAGAAACTGAAGTGGCCAGAACCTGCTAAATTCAAGCTGAGTGAAGTGGAAAGGCCCTGT
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCTTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTGAUTCAGCAAGAAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCCTGCTTCTAAAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGGLAEVSKVAEQVLNAVNKGLYRE
ATELGWGKAEMIIEQNTDGVNFYNILTGSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355,
449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGATCGTGGGTGGAGAGGACGCCAACTCGGGCGTTGGCGTGGCA
GGGGAGCCTGCGCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCAC TGCTTGA AACCTATAGTGACCTAGTGATCCCTCCGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCCTGTCTCCAG
GCCTCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTGCCATCATAACA
ACTCTATGTGCAACCACCTCTTCCCTCAAGTACAGTTCCGCAAGGACATTTGGAGACATG
GTTTGTGCTGGCAACGCCAACGGGGAGGATGCCCTGCTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTACACCAATATGCCACCACTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCTGGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGG
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEELGRWPWQGSLRLW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSSGPLACNKNG
LWYQIGVVSWGVCGRPNRPGVYTNISHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACCGCGTCCGGACCGGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCCGAGCCCACCGCGGAGGACGC
TGCCCCCAGGCTGGGTGCCCTGGCGTGCGGACCCCTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAAATGTGGAAAGACTCTCGGAGCTGGTGCAAGCTGTGTCGGATCCCAG
CTCTCCTCAATAACGGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCCTCACACGGTCAAAAATGGCTTGGCAGCCGAGCCCAGAAGTGCCTATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTCCACAGGCCTTGGCCCCCATGTGGACTTGTGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGCAAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCTCTGTGATCCGTAAGCGATACAACCTGACCTACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTTCATGCCTCTCGGTGGCAACTTGCACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCA
ACCTGATGAGTGCTGGTCCAACATCTCACCTGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTCTGCACTGGCTCATGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGGCCACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCCTCGGGTCTCACCCCTGCTTTCGCCCTCAGGTGACAGT
GGGGCCGGGTTGTTGGTCTGTCTGGAAAGACACCAGTCCGCCAACCTCCCTGCCCTCCAG
CCCCTATGTCACCACAGTGGGAGGCACATCCTCAGGAACCTTCCTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCTCATACCAGGAG
GAAGGCTGTAACGAAGTTCTGAGCTCTAGCCCCCACCTGCCACATCCAGTTACTCAATGC
CAGTGGCGTGCCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGGCCATTCCATGGGTGTCCGAACCTCGGCCTCTACTCCAGTGTGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCCCCCCTCTGGCTTCTCAACCCAAG
GCTTACCAAGCAGCATGGGCAGGTCTTTGATGTAACCGTGGCTGCCATGAGCCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGCTGGATCCTGTAACAGGC
TGGGGAACACCAACTTCCCAGCTTGCTGAAGACTCTACTCAACCCCTGACCCCTTCCTATC
AGGAGAGATGGCTGTCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATTCTGCCCTTTG
GAAGCCCTGCTGAACCTCAACTATTGACTGCTGCAGACAGCTTACTCCCTAACCTGAAA
TGCTGTGAGCTTGACTTGACTCCCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCTTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGATGCTCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGCTTCCAAAGGGTTGTATAAGACTCTGTGCACTA
TTTCACCTGATATTCACTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTCTCAATCTTGTCTTATG
GCCTTCCATCATAGTTGCCACTCCCTCTCCTTACTTAGCTCCAGGTCTTAACCTCTCTG
ACTACTCTTGCTTCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTGC
TCCATTGTAGATTTGCTCTCAGTTACTCATTGTCCCTGGAACAAATCACTGACA
TCTACAACCATTACCATCTCAACTAAATAAGACTTCTATCCAATAATGATTGATACCTCAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSPHYQLPQALAPHVDFVGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDEDLSAYIQRVNTELMKAAARGLTLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHECLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCTCCGGGCCACACCTGTCTGAGCGGCGCAGCGAGGCCGGCCGGC
GGGCTGCTCGCGCGGAACAGTGCTGGCAGGGATTCCAGGGCTCCTTCCTCTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATACCGCCTCCCTGCGTCTGGCCCAGTCTACCCCTAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCCAGTGTATAAGGAACT
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAAAGGACTTCCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACGATGTCCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTCGAGTGGCTTCCTAAAGCCC
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGCTAACAGCTGCCAGGGGCAGAATTCACTTCTC
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCCTACCAAGCAATGCGATGCCAGCCAGGGGCCAGCGGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGCAGAAGTGGAGCGAAAAATTATTGGCATTTCAGG
GCACCAAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGGCTCTGGCAGCAATTAGGGCTTCATGTTCTTATTTAGGAGAGGCC
AAATTGTTTTGTCTGGCGTGCACACGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAATACTGATTGGGCAATGAGGAATATTGACAATTAGTTAATCTCACGTTTG
CAAACTTGATTTATTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLQSTLNLA
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAACIH
TQKLRVGFLKPDKFDGGRGANDSTSAMPEQMFKQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYD
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320,
338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGGTCTCTGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCCAGCCCTGGTGGGGCTGTCTCGGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCAGCCTGTGGAAAGCCCCA
GCAGCTGAACCGGGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCCTGCGCAGGTTCTGCTCACCAAGCCCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTCGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCCTGTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCAGGCTCTGCCCACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCCTCAGACCCCTGCAGAACGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCCACTCCGGGGCCCCCTATGTGCCAGGTGGACG
GCGCCTGGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCTGGTGGAGAAGATCGTCAAGGGTGCA
GCTCCCGGGCGCCTCAGGGGGTGGGCCACTGGGACCCCTCAGGGCACCAGGGCTCTGGGCC
CCGCGCGCTCCTAGGGCGCAGCGGGACCGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGGGGCGGCTCGGGCGGTTTCCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTCGGAAAGGAAACCCCTCCCCGACCGCCGAC
GGCCTAGGCCCTCCAAGGCATCAGGCCCGCCAACGGCCTCATGTCCCCGCCAC
GACTTCCGGCCCCGCCCGGGCCCAAGCGCTTTGTGTATATAAATGTTAATGATTTTAT
AGGTATTGTAACCCTGCCACATATCTTATTATTCTCCCAATTCAATAATTATTATT
CTCCAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLF SVLLGAWQLGNPGSRQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPI CLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459,
528-534, 612-618, 623-629, 714-720, 873-879

FIGURE 99

ACGGGCTGCCACCAATGCACGGCTCCTGCAGTTCCCTGATGCTTCGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGCCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCCTCGCCAAGGCCCTACGCACGGCAGTGCCTGGGCCAC
AACAAAGGAGCGCGGGCGCCGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCCACTACACGCAGGTGGTATGGCCAAGAACAGAGAGGATC
GGCTGTGGTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCCTCCAAATGTCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCCTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTCCCTAGCAACGGGATTCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCGTGTTGAAACCCAGGCC
CCAACCTCCTAGCAACGAAAGACCCGCCCTCATGGCAACAGAGGCTCACCTGCGTAAC
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGGCCAGTTA
CCTTCCCCAAATCGACCCATGTCCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCTGACAGGGCAAG
GGAACCTCCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCTCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCCTGCCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTCAGGGCTGAACCTGGCCCTGGTCATGTTGGGGCCCTCCTGGGA
CTACTGCTCCTGCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCAACTCAAAGGG
TGAAGAGGTAGCTGTCCTCTGTCATCTTCCCCACCCCTGCCCCAGCCCTAAACAAGATA
CTTCTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGCATGTCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTGCCCTCCCTGAGTCCTGGGGTGGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACGATGTCGCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTTC
TTTGAGTGGGGAGGCAGGGACGAGGAAGGAAAGTAACCTGACTCTCCAATAAAAACCT
GTCCAACCTGTGAA

FIGURE 100

MHGSCSFLMLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMVDPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGETPCSQC
PSGYHCKNSLCEPIGSPEADAQDLPYLVTTEAPSFRATEASDSRKMGTTPSSLATGI
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTVPSPRSPEAQLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186,
231-237, 250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTGAAAGTCAGGCTTTCAATTGGGAAGCCCCCTCAACAGAATTGGTCATTCTCCAAGTTATGGTGGACG
TACTTCTGTTCTCCCTTGCTTACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTC
ATCAAGGCAAGTCCATGAGCCACCTCAAAGCCTCGAGAAGTGAACACAATGAATTGGAGACCCT
TCCAAATCTGGGACCAGTCTCGCAAATATTACACTTCTCTCCCTGGCTGGAAACAGGATTGGAAATACTCC
CTGAACATCTGAAAGAGTTCAAGTCCCTGAAACTTGGACCTTAGCAGCAACAATATTCAGAGCTCCAAACT
GCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCACACAGAACCGAGTCACATCAATGGAACCTGGGTATTT
TGACAATTGGCCAACACACTCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAGATGT
TTAAACTGCCCAACTGCAACATCTCGAATTGAACCGAAACAGATTAAAAATGTAGATGGACTGACATTCCAA
GGCCTGGTCTGCTGAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGG
GCTGAGCAACATGGAATTTCAGCTGGACATAACAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCT
TGCTGATGCTGAGGAACTTCATCTCAGCCTAAAGGATCAGGCTGAGCTTACGGCTTACGGCT
CAGAAGCTCAGTGAAGCTGGACCTAACATTCAATCAGGTTAGATGATTCAAGCTTCCCTGGGACTTCCAA
CTTACTAAATACACTGCACATTGGAACACAGAGTCAGCTAACATTGCTGATTGTGCTTCCGGGGCTTCCA
GTTAAAGACTTGGATCTGAAGAACATGAAATTCTGGACTATTGAAGACATGAATGGTGTCTTCTGGG
CTTGACAAACTGAGCGACTGATACTCCAAGGAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTT
GGATGCAATTGGAGCATCTAGACCTGAGTGACAACGCAATCATGCTTTACAAGGCAATGCAATTTCACAAATGA
AGAAACTGCAACAATTGCAATTAAATACATCAAGCCTTTGTGCGATTGCCAGCTAAATGGCTCCCACAGTGG
GTGGCGAAAACAACCTTCAGAGCTTGTAAATGCCAGTTGTGCTTCCAGCTGCTAAAGGAAGAAGCAT
TTTGCTGTTAGCCCAGATGGCTTGTGATGATTTCACAGGCTTACGGCAATGCAATTTCACAAATGA
AGTCGGCAATAAGGTTCCAATTGAGTTTCACTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTT
GCTTGGAAAAAGACAATGAACACTGCACTGATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCAAGGTGG
CGAGGTGATGGAGTATACCACCATCCTCGGCTGCGAGGTGGAATTGCCAGTGAGGGAAATACAGTGTG
TCATCTCAATCACTTGGTCATCTACTCTGCTAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCA
AAGACCCCCATGGATCTCACCACCGACTGGGGCATGGCACGCTGGAGTGTGCTGCTGGGGCACCCAGC
CCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGACTTCCCACTGCAACGGGAGAGACGCATGCATGTGATGC
CCGAGGTGACGTGTTCTTATCGGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCAAGCTCAGAAC
AGTGAGGAAGTATTCAGCAATGCAACTCTGACTGCTCTAGAAGAACACATTTTGCAGGCACTGTTGG
CCGAACACTGAAACAGGGAGAACACGGCGCTCTACAGTCAGTGTGGAGGAAGCCCTCCCCCTAAACTGAAC
GGACCAAAGATGATAGCCCATTGGGTTAACCGAGAGGCACTTTTGCAAGCAGGCAATCAGCTCTGATTATT
GTGGACTCAGATGTCAGTGATGCTGGAAATACACATGTGAGATGTCTAACACCCCTGGCACTGAGAGAGGAA
CGTGCCTCAGTGTGATCCCCACTCCAACCTGCACTCCCTCAGATGACAGCCCCATCGTAGACGATGACG
GATGGGCACTGTGGGTGCGTGTGATCAGCCGTGGTTGCTGTGGGGCAGTCAGTGTGGGTGGC
ATCATATACCACACAAGGGAGGAATGAAGATTGCACTACCAACACAGATGAGACCAACTTGCAGCAG
TATTCTAGTTATTGTCATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGCTTCA
GCCACCACAGTTGTCACATCTCAGGTGCTGGATTTCACACATGACAGTAGTGGGACCTGCCAT
ATTGACAATAGCAGTGAAGCTGATGGAAGCTGCCACAGATCTGTTCTTGTCCGTTTGGGATCCACAGG
CCCTATGTATTGAAGGGAAATGTGATGGCTCAGATCCTTTGAAACATATCATACAGGTTGCA
CAAGAACAGTTTAATGGACCACTATGAGCCAGTTACATAAAGAAAAGGAGTGTACCCATGTTCTCATCCT
TCAGAAGAATCCTGCCAACGGAGCTCAGTAATATATCGTGGCCTCACATGTGAGGAAGCTACTTAACACTAG
TTACTCTCACAATGAAGGACCTGGAATGAAAATCTGTGCTAAACAAGTCTCTTACGTTAGATTGCAAATC
CAGAGCCAGCGTGGCTGCTCGAGTAATTCTTCATGGTACCTTGAAAAGCTCAGGGAGACCTCACCTA
GATGCCATTCAAGCTTGGACAGGCCATCAGATTGTCAGCCAAGGCCCTTATTGAAAGCTCATTCTCCCC
AGACTGGACTCTGGGTGAGAGGAAGATGGAAAGAAAGGACAGATTTCAGGAAGAAAATCACATTGTACCT
TTAACACAGACTTAAAGAAAACAGGACTCCAATTTCAGTCTTACGTTAGACGTTGGACACATAGACTGAATGAGAC
CAAAGGAAAAGCTTAACACTACCTCAAGTGAACCTTTATTAAAAGAGAGAGAATCTTATGTTTAAATG
GAGTTATGAATTAAAAGGATAAAATGCTTATTATACAGATGAACCAAATACAAAAGTTATGAAAAT
TTTATACGGGAAATGATGCTCATATAAGAACATCCTTTAAACTATTGTTATAATGCCAGATTCTTTATGGA
AAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCATTTTAAATAGAAGTTACTCATTATATT
TTGCACATTATATTAAATAAAATGTGTCATTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRI SAI PPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE
FCQKLS ELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDLKNE
ISWTIEDMNGAFSGLDKLRRLI LQGNRIRSITKKAKFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQQLHLNTSSLLCDCQLKWLPQWVAENNQSFVNASC AHPQLLKGRS IFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGH PAPQIAWQKDGGTDFPAARERRMHVPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVKGETAVLQCIAGGSPPP KLNWTKDDSPLVVTER
HFFAAGNQLLIIVDSDVSDAGKYTC EMSNTLGTERGNVR LSVIPTPTCDSPQM TAPS LDDDG
WATGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGT LAD
RQDG YVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDPFETYHTG CSDPRTVLMHYEPSYIKKKECYP CSHPSEES CERSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTL ENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459,
528-534, 612-618, 623-629, 714-720, 873-879

FIGURE 103

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLVLLALQLLVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFNDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLLRDLGELKRLS
YISEGAFEGLSNLRYLNLMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWCNCIDL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN
TTASATLNVTAATTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTPMESHPMPAIHEHHLNHYN SYKSPFNHTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTCGGTTCCCTGCTGTTGGGGC
ATGAAAGGGCTTCGCCGCCGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCAGCGAC
GCGAGGGCGGCGTGCACCCCTCGGCTGGAAGTTGTGCCGGCCCCGAGCGCGCGCCGGCTGGAGCTCGGGT
AGAGACCTAGGCCGCTGGACCGCG**AT**GAGCGCGCCGAGCCTCCGTGCGCGCGCCGGGGTTGGGCTGCTGCT
GTGCGCGGTGCTGGGCGCGCTGGCGGTCCGACAGCGCGGTGCGGGAACTCGGGCAGCCCTCTGGGTAG
CCGCCGAGCGCCCATGCCCACTACCTGCCGCTGCCCTGGGACCTGCTGGACTGCACTGTAAGCGGCTAGCG
CGTCTTCCCAGGCCACTCCGCTGGCGTGGACTTAAGTCACAACAGATTATTTCATCAAGGC
AAGTTCCATGAGCACCTTCAAAGCCTTCGAGAAGTGAACAAACAATGAATTGGAGACCATTCAAATC
TGGGACCAAGTCTCGGAAATATTACACTCTCTCCGGCTGGAAACAGGATTGTGAAATACTCCCTGAACAT
CTGAAAGAGTTCTGAACTTGGACCTAGCAGAACAAATTTAGCAGGAGCTTACAGCTTAACTG
AGCCCTACAGCTCAAATATCTGTATCTCAACAGAACCGAGTCACATCAATGGAACTGGGTATTTGACAATT
TGGCCAACACACTCTTGTTAAAGCTGAAACAGGAACCGAATCTCAGTATCCCACCCAAAGATGTTAAACTG
CCCCAACTGCAACATCTGAATTGAAACCAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCCTGG
TGCTCTGAAGTCTGAAAATGAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCA
ACATGGAAATTTCAGCTGGACCATAACAAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGATG
CTGCAGGAACCTCATCTCAGCAAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAGCT
CACTGAGCTGGACCTAACCTCAATCAGTTGAGATGATTCAAGCTTCTGGCTAACAGCTTAAAG
ATACACTGCACATTGGAAACACAGAGTCAGCTACATTGCTATTGTGCTTCCGGGGCTTCCAGTTAAAG
ACTTTGGATCTGAAGAACATGAAATTCTGGACTATTGAAGACATGAATGGTGTCTTCTGGCTTGACAA
ACTGAGGGGACTGATACTCCAAGGAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCA
TGGAGCATCTAGACCTGAGTGACAACGCAATCATGTCTTACAAGGAATGCATTTCACAATGAAGAAACTG
CAACAATTGCAATTAAACATCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGGA
AAACAACCTTCAGAGCTTGTAATGCCAGTTGCCCCATCTCAGCTGCTAAAAGGAAGAACATTTGCTG
TTAGGCCAGATGGCTTGTGATGATTTCCAAACCCAGATCACGGTTCAGCCAGAACACAGTCGGCA
ATAAAAGGTTCAATTGAGTTCATCTGTCAGCTGCCAGCAGCAGTGTGATCCCCAATGACTTTGCTGGAA
AAAAGACAATGAACACTACTGCATGATGCTGAAATGGAAATTATGCACACCTCCGGGCAAGGTGGCGAGGTGA
TGGAGTATACCACCATCCTCGGCTGCGAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCC
AATCACTTGGTCATCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCC
CATGGATCTCACCATCCGAGCTGGGCCATGGCACGCTTGGAGTGTGCTGTGGGCCACCCAGCCCCCAGA
TAGCCTGGCAGAAGGATGGGGCACAGACTTCCAGCTGCACGGAGAGACGCATGTGATGCCGAGGAT
GACGTGTTCTTATCGTGGATGTGAAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTCAGG
AAAGTATTTCAGCAAATGCAACTCTGACTGTCTAGAAACACCATATTGGCAGGCCACTGTTGGACCGAACTG
TAACCAAGGGAGAACAGCGCTTACAGTCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAA
GATGATAGCCCATTGGTGTAAACCGAGAGGCACTTTTGCAAGCAGGCAATCAGCTCTGATTATTGTGACTC
AGATGTCAGTGTGCTGGAAATACACATGTGAGATGTCTAACACCTGGCACTGAGAGAGGAAACGTGCGCC
TCAGTGTGATCCCCACTCCAACCTGCACTCCCTCAGATGACAGCCCCATCGTAGACGATGACGGATGGGCC
ACTGTGGGTGTCGTGATCATGCCGTGGTTGCTGTGTTGGCACGTCACTGCTGGGTGGTCATCATATA
CCACACAAGGCGGAGGAATGAAGATTGCACTTACAAACACAGATGAGACCAACTTGCAGCAGATATTCC
GTTATTTGTCATCTCAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGCTTCAAGAAAGTGGAAAGCC
CAGTTTGTACATCTCAGGTGCTGGATTTCACACATGACAGTAGTGGACCTGCCATATTGACAA
TAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTCCCTTGTCCGTTGGATCCACAGGCCCTATGT
ATTGAAAGGGAAATGTGATGCTCAGATCCTTTGAAACATATCATAACAGGTTGCACTGCCTGACCCAGAAC
GTTTAATGGACCACTATGAGCCCAGTTACATAAAAGAAAAAGGAGTGTCACTTACATCTCAGAACAG
ATCCTGCAACCGAGCTTCACTGAAATATGCTGGCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTC
AACATGAAGGACCTGGAAATGAAAATCTGTCTAAACAGTCTTACAGGAAAGGAGCTTACAGTGGAC
GGCTCGGGTGCCTCGAGTAATTCTTCATGGGTACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCC
TTCAAGCTTGGACGCCATCAGATTGTCACTGCCAGAGCTTACAGGAAAGGAGCTTACAGGAAAG
ACTCTGGGTCAAGAGGAAAGGAAAGGAGCTTACAGGAAAGGAGCTTACAGGAAAGGAGCTTACAGGAAAG
ACTTTAGAAAATCAGGACTCCAAATTTCAGTCTTATGACTTGGACACAT**AG**ACTGAATGAGACCAAGGAA
AAGCTTAACATACTACCTCAAGTGAACCTTATTAAAAGAGAGAGAATCTTATGTTTTAAATGGAGTTATG
AATTTAAAAGGATAAAAATGCTTTATTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTATAC
TGGGAATGATGCTCATATAAGAATACCTTTAAACTATTTTAACTTTGTTATGAAAAAAAGTATCTTAC
GTAAATTAAATGATATAATCATGATTATTTATGATTATTTATAATGCCAGATTCTTTATGGAAAATGAGT
TACTAAAGCATTAAATAAATACCTGCCATTGTAACCTTTAAATAGAAGTTACTTCATTATTTCCACAT
TATATTAAATAAAATGTGCAATTGAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAEERPCPTTCRCLGDLLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSA
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRV
TSMEPGYFDNLANTLLVLKLNRRNRI
SAI
PPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMGDGAFWGLSNMEILQLDHNNLTEITKGWL
YGLLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRV
SYIADCAFRLSSLKTL
DLKNNEISWTI
EDMNGAFSGLDKLRRLILQGNRIRSITKAFTGL
DALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNTSSLLCDCQLKWL
PQWVAENNQSFVN
ASCAHPQLLKGRSIFAVSPDGVCDDF
PKPQITVQPETQSAIKGSNLSFICSA
ASSSDSPMTFAWKDNELLH
DAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQC
VISNHFGSSYSV
KAKLTVNMLPSFTKTPMDLT
IRAGAMA
RLECAA
VGHPAPQIAWQKDGGTDFPA
ARERRMHVMPE
DDVFFIVDV
KIEDIGV
YSC
TAQNSA
GSISANATLTV
LETPSFLRPLL
DRTVTKGETAVL
QCIAGGS
PPP
KLN
WTK
KDD
SPLVV
TERHF
FAAGNQLLI
IVDSDVSDAGKYTC
EMSNTLG
TERGNV
RLSVI
PTPTCDSPQM
TAPS
LDDDGWA
TVGVVI
IAVVCCV
VGTSL
VVVII
YHTRRR
NEDCS
ITNT
DET
NLP
ADI
PSYL
SSQ
GT
LADRQ
DGYVS
SES
GSH
HQF
VTSS
GAG
FFLP
PQHD
SSGT
CHID
NS
SEAD
VEA
ATDL
FLCP
FLG
STGP
MY
LKGNV
YGS
DPF
ETY
HTGC
SPDP
RTV
LMD
HYEP
SYI
KK
KEC
YPC
SHP
SE
ESC
ERS
FSN
IS
WPS
HVR
KLL
NTS
YSH
NEG
PGM
KNL
CLNK
SSL
DFS
ANPE
PAS
VASS
NSFM
GTFG
KAL
RRPH
L
DAYS
SFGQ
PSDC
QPR
AFYL
KAH
SSP
DLS
GSE
EDG
KERT
DFQE
ENHI
CTF
KQT
LEN
YRTP
NFQ
SYD
LDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473,
515-519, 688-692, 729-733, 905-909, 987-991, 999-1003,
1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328,
374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713,
731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007,
1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGCGAGAGCGCCCAGCTGACTTGAATGGAAGGAGCCCGAGCCCGCGAGCGCAGCTGAGA
CTGGGGGAGCGCGTTCGGCCTGTGGGGCGCGCTCGCGCCGGCGCAGCAGGGAAAGGGAAAGCTGTGGTCTG
CCCTGCTCCACGAGGCACACTGGTGTGAACCGGGAGAGCCCCCTGGGTGGTCCCCTATCCCTCCTTAT
ATAGAAACCTTCCACACTGGGAAGGCAGCGCGAGGCAGGGCTCATGGTGAGCAAGGAGGCCGCTGATCT
GCAGGCGCACAGCATTCCGAGTTACAGATTTACAGATACCAATGGAAGGCAGGGAGGCAGAACAGCCTGC
CTGGTTCCATCAGCCCTGGCGCCAGGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGCCGGG
TGCTGCTGCTCTGCTGCTGCCACAGCTGCACCTGGGACCTGTGCTGCGTGAGGGCCCCCAGGATT
GGCGAAGTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTGCGGAGGAGGCCGGTGTGGTACTGAG
CCCTGAGGAGGCCGGCCCTGGCCAGCCCGGTCAGCTGCCCGAGACTGTGCCGTGGTCCAGGAGGGCGTCG
TGGACTGTGGCGGTATTGACCTCGCTGAGTTCCCGGGGACCTGCTGAGCACACCAACCACCTATCTCGCAG
AACAAACCAGCTGGAAAAGATCTACCCCTGAGGAGCTCCCGGCTGGAGCACACCAACCTCAATTACCTGTACTGG
CCAATAACAAGCTGACCTTGGCACCCCGCTTCTGCCAACCCCTGATCAGTGGAACCTTGCTGCCAACTAT
CTCACCAAGATCTATGGGCTCACCTTGGCCAGAAGCAAACCTGAGGTCTGTGACCTGCAACAACAAGCT
GGCAGACGCCGGGCTGCCGACAACATGTTAACCGCTCCAGCAACGTCGAGGTCTCATCCTGTCCAGCAACT
TCCCTGCCACGTGCCAACGACCTTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTC
GGGCTGGACAACGAGACCTCTGGAGCTCTGGAGCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTC
GGGTCCCAGCTGGGCTGCCGCGAGCCTGGTGTGCACTGGAGAAGAACGCCATCCGGAGCGTGGACGCG
AATGTGCTGACCCCCATCCGAGCCTGGAGTACCTGCTGTCACAGCAACCAGCTGGGAGCAGGGATCCA
CCCACTGGCCTTCAAGGGCCTCAAGCGGTTGCACACGGTGACCTGTACAACAAACCGCCTGGAGCGCGTGGCCA
GTGGCCTGCCCTGCCGCGTGCACCCCTCATGATCCTGCAACACCAGATCACAGGATTGGCCGGAAGACTTT
GCCACCAACTACTTCTGGAGGAGCTAACCTCAGCTACAAACCGCATCACCAGCCACAGGTGCACCGCGACGC
CTTCCGCAAGCTGCCCTGCGCTCGCTGGACCTGCGACCGCCTGGAGTACCTGGCTGCCACAGCTGCCACCTGGCTGC
CTCGAAATGTCCATGTGCTGAGGTCAAGCGAATGAGCTGCTGCCACAGGAGGGCGCTGGCGGGCATG
GCTCAGCTGCGTGAAGCTGTACCTCACCAGCAACCCACTGCCAGCCGAGCCCTGGGCCCCCTGCGCTGGTGG
CCTCGCCCATCTGCACTGCTGGACATGCCGGGAATCAGCTCACAGAGATCCCCAGGGCTCCCCGAGTCAC
TTGAGTACCTGACTCTGAGAACAAAGATTAGTGGGGTGGCCCAATGCCCTTGACTCCACGCCAACCTC
AAGGGGATCTTCTCAGGTTAACAAAGCTGGCTGGGCTCCGTGGTGACAGTGCTTCCGGAGGCTGAAGCA
CCTGAGGTCTGGACATTGAAGGCAACTTAGAGTTGGTGACATTCCAAGGACCGTGGCCCTGGGAAG
AAAAGGAGGAGGAGGAAGAGGAGGAGGAGGAAGAGGAACAAAGATAGTGACAAGGTGATGCAAGATGTGACC
TAGGATGATGGACGCCGGACTTTCTGCAACAGCCTGTGCTGTGAGCCCCCACTCTGCCGTGCTC
ACACAGACACACCCAGCTGCACACATGAGGCATCCCACATGACACGGGTCACAGCTCATATCCCCACCCC
TTCCCACGGCGTCCCCACGCCAGACACATGCACACACATCACACCCCAAACACCCAGCTGCCACACACA
ACTACCCCTCAAACACCACAGTCTGTGACACCCCCACTACCGCTGCCACGCCCTGTAATCATGCAGGGAA
GGGTCTGCCCTGCCCTGGCACACACAGGCACCCATTCCCTCCCCCTGTCAGATGTGATGCGTATGCATACA
CACACACACACACACATGCACAAGTCATGTGCAACAGCCCTCAAAGCCTATGCCACAGACAGCTTGTGCC
CAGCCAGAATGCCATAGCAGCTGCCGTCTGCCCTGTCATCTGCGCTGCCCTGGAGAACACACAAG
GGTATCCATGCTCTGGCCAGGTGCCACCCCTGGAACACTACAAAAGCTGGCTTTATTCTTCCAT
CCTATGGGACAGGAGCCTCAGGACTGCTGCCCTGCCACCCCTGCTCCAGGTGCTGGCAGT
CJ CTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACACAGGCACTTTCCAATGGCAAGCCCAGTGGAGG
CAGGATGGAGAGGCCCTGGGTGCTGCTGGGCTTGGGAGGACTGAAGCAGAGGTGATGGGCTGGCTG
AGCCAGGGAGGAAGGACCCAGCTGACCTAGGAGACACCTTGTCTCAGGCCCTGTTGGGGAAAGTTCCGGTGC
CCTTATTTTATTCTTAAGGAAAAAAATGATAAAATCTAAAGCTGATTTCTGTTATAGAAAAAA
CTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENFAEEEPLVLSPEEPGPAAVSCP RD CACS QEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKA FEHLTNLYLYL ANNK
LT LAPRFLPNALISVDFAANYLT KIYGLTFGQKP NLRSVYLHNNKLADAGLPDNMFNGSSNV
EV LILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPA GLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLP RRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITS PQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEAALA
RGALAGMAQLRELYL TSNRLRSRALGPRAWV DLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANA FDSTPNLKGIFLRFNKLAVGSVVDSA FRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242,
335-341, 477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486,
471-493, 535-557

FIGURE 109

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGEICGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSGHLAPDGRTCDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMIIGGKYQCHDIDECSLGQYQCSSFARCYNRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPTELRTPLPPTPERPTGLTTIAPAASTPPGGITVDN
RVQTDPQKPRGDVFSLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAQQYLTVAAKAPGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227,
236-242, 421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTCGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTCACAACTTCCCTTGCAACAGGTGCTCGCTGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAAGAGGTCAAGGCCCTACCTACCGTC
CACTATGGCTCCACACTCCAGCATCAGACATCCAGATCATGGCTATTGAGAGACCCCA
CACAATGCCAAATACTACTGGCTCTGTGAATAAGTCTGTGGTCCCTGACTTGAATACC
AACACAAGTCACCATGATGCCACCAATGCATCTGCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAAGGAAATGGAACACTATCTGCCAGTCA
GAAGATACAAGTCACGGTGATGATCCTGTCACAAAGCCAGTGGTGCAGATTCACTCCCT
CTGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAGGGGACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCACACCAGCTCCACCTACTCCTTTC
TCCCCAAACAATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCTGTCAGTGAAATGGAAAGTGATATCATTATGCCATCATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTACTGT
TGACCTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGAAGTGCACAAACTACATATCATTAAGCATGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAACAGAACATGGACTATGTGTGCTGCTACAACAAACATAAC
CGGCAGGCAAGATGAAACTCATTTCACAGTTATCATCACTCCGTAGGACTGGAGAACGCTTG
CACAGAAAGGAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATTTGATT
ATATCCATGTGTCTTCTCTTCTATGGAAAAAATATCAACCTACAAAGTTAAAACAGAA
ACTAGAAGGCAGGCCAGAACAGAACATCAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTGTTCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATGGCAAGTATAACTGGAATATCA
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGAACAGACATCCAGAGTGAACATTTCATGG
GCTAAACAGTACATTCAAGTGAAGAAACACCAGGACCAACACCTCTTACTCATTATTCTTACA
TGCAGAATAGAGGCATTATGCAAATTGAACACTGCAGGTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGTTCTCATAGTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTACATTGTCGATTTCAGCAGACTTGTATTAAATTTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTATTCAAATTCTATCTGTATTGTACAA
CAAAGTAATAAGGATGGTGTCAACAAAACAAAATATGCCTCTQTTTTTCAATCACC
AGTAGTATTGGAGAAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA
TTTTTCAAGGAAAGATGGATTCAAATAAAATTATTCTGTTTGCTTTAAAAAAAAAAAA
AA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLSASQ
KIQVTVDDPVTKPVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430,
433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTCAGTCCCCCTGGCAGTCCTGGTGTGTT
GCTTGGGGTGCCTCCCTGGACGCCACGGCGGAGCAACGTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTATGCCCGTGGTGCCCCTGCT
TGTCAAAAATCTCAACCAGGAATGGGAAAGTTGCTGAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTATCATGTAAAGATGGGAATTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCCATAAAACTTATAAGTGATAAAGAGTGGAGAGTATTGAGCCCGTTCATCATG
GTTTGGTCCCAGGTTCTGTTGATGAGTAGTATGTCAGCACTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTATTGAAAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGACTGTTATTAGGACTCTGTATGATATTGTCGC
AGATTGCCTTGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAAAT
TATTATCAGAACTGCACAACCTTGAAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTCAGAAGAAGAAGCTGAAAGTAAAGAACAAACAAAGACTTCCACAGAAATGC
CATAAGACAACGCTCTGGTCCATCATTGCCACAGATAAACTCTAGTTAAATTTATAG
TTATCTTAATATTATGATTTGATAAAACAGAAGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAAATTGCAAGGTTCAGCTAGATTGTATAAATGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTTACAGTTGAAATATGATTAAAGCACAGTATGATG
GTTAAATAGTCTCTAATTGAAATCGTGCCAAGCAATAAGATTGTATATTGT
TTAATAATAACCTATTCAAGTCTGAGTTGAAAATTACATTCCAAGTATTGCATTAT
TGAGGTATTTAAGAAGATTATTTAGAGAAAAATATTCTCATTGATATAATTTTCTCTG
TTTCACTGTGTGAAAAAAAGAAGATATTCCCATAAAATGGAAGTTGCCATTGTCTCAAG
AAATGTGTATTCACTGACAATTCGTGGTCTTTAGAGGTATATTCCAAATTCTGT
ATTTTTAGTTATGCAACTAAAAAACACTTACATTAATTAAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTAAGTTCATGGTATTCTTGTGATT
CAACAAAGTTGATTTCTCTGTATTCTACTATGGGTTACATTTTATTTTGT
CAAATTGGATGATAATTCTGGAAACATTTTATGTTAGTAACAGTATTTTGT
GTTTCAAACTGAAGTTACTGAGAGATCCCATCAAATTGAACAACTGTTGTAATTAAAATT
TTGGCCACTTTTCAGATTTCACATCATTCTGCTGAACTTCAACTGTGAAATTGTTTTT
TTTCCTTTGGATGTGAAGGTGAACATTCTGATTTTGTGATGTGAAAAGCCTGGTA
TTTCACATTGAAATCAAAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAG
CATCTCTTGATATGCTTAATGTATTTTGCTCTCATATACAGAAAGTCTTAATTGAT
TTTACAGTCTGTAATGCTGATGTTAAAATAACATTTTATTTTAAAGACAA
ACTTCATATTACCTGTGTTCTCCTGACTGGTAATATTGGTGGGATTTCACAGGAAAAG
GTCAGTAGGATGGAACATTAGTGATTTTTACTCCTAAAGAGCTAGAATACATAGTT
CACCTTAAAGAAGGGGAAATCATAAAATACAACTGAATCAACTGACCATTACGTAGTAGAC
AATTCTGTAATGTCCCCTTCTTCTAGGCTCTGTTGCTGTGAAATCCATTAGATTACAG
TATCGTAATATAACAGTTCTTAAAGCCCTCTCCTTAGAATTAAAATATTGTACCATT
AAAGAGTTGGATGTGTAACTGTGATGCCTTAGAAAAATATCCTAAGCACAAAAAACCT
TTCTAACCACTCATTAAAGCTGAAAAAAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIKVADCLCPSKRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNPAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTATAATTGTTAACTAATTCAACAAACGGGACCCTT
CTGTGTGCCAGAAAACCGCAAGCAGTGTGCTAACCCAGTGGGACAGGGGGATTGGAAGAGCGGG
AAGGTCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACC**ATGAAACTCTGGGTGTCTGC**
ATTGCTGATGGGCTGGTTGGTCTGAGCTGTGCGAGGCCAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGGCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCCCTGTGAATGCCTACAAACTGG
TGAAGCGGCTAACACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCGAGGACTCAGCTGCA
GGTTTATCGCCAACCTCTGTGCGAGCGGCAAGTCTTCCCCACTGATGAGGAGCAGGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGAACTTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCGCTCGGCCAACATGAAGGGGACTATTATCATACGGTGTGATGGAGCAGGTGCT
AAAGCAGCTTGTGATGCCGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGTCTCCAGTTGGGTGATCTGACCGTGCCTGGAGCTCACCCGCCGCTGCTC
TCCCTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAGAAGGCA
TCTATGAGAGGCCCTGTGACTACCTGCTGAGAGGGATGTTACGAGAGCCTCTGCGTGG
GAGGGTGTCAAACGTACACCCCCTAGACAGAAGAGGCTTTCTGTAGGTACCAACCATGGCAA
CAGGGCCCCACAGCTGCTATTGCCCTCAAAGAGGAGGAGCAGTGGACAGCCGCACA
TCGTCAGGTACTACGATGTCATGTCAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTTGACGAGCACCCTCGTGTGATCCAAGACAGGAGTCCTCACTGTCGCCAGCTA
CCGGGTTCCAAAAGCTCTGGCTAGAGGAAGATGATGACCCCTGTTGCGCCAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGAGGACAGTATGAACCGCACTCGACTTCTCTAGGGCACCTTGTACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAGCTG
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTTGCAGGGAGCAGGAAAGGTGACTACCGAACAGACATGCTGCC
TGTGCTGTGGCTGCAAGTGGGTCTCCAATAAGGGTCCATGAACGAGGAGCAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGTTGACT**GACATCCTTCTGTCTCCCTGGTC**
CTTCAGCCCAGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCTGT
GTGACTGAAGTCCCAGCCCTCCATTGACCTGCTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTT
TTAGGTGTGAGATGTTCAAGTGAACCAAAGTTCTACACCTTGTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAAATAAAATGTCCTACAGAAAAAAAAAA

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FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWALEDLVLQDSAAGFIANLSVQRQFFF
TDEDEIGAAKALMRLQDTYRLDPGTISRGEPLGTYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLKQLDAGEEATTKSQVLDYLSYAVFQLGDLHRALELTRRLLSLDPSPHERAGGNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVVDYLPERDVYESLCRGEGVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIYRYYDVMDSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDGSLKTEGNRLATFLNYMSDVEAGGATVPDLGAAIWPKKGTAVFWYNLLRSGEGDYR
TRHAACPVVLVGCKWVSNKFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE.117

GCAGTATTGAGTTTACTTCCTCCTTTAGTGGAAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTG
TTTCATTATTACCGTTGGCTGGGGTTAGTCCGACACCTCACAGTTGAAGAGCAGGCAGAAGGAGTTG
GAAGACAGGACAATCTCTGGGATGCTGGTCTGGAAGCCAGCAGGGCTTGCTCTGTCTTGGCCTCATTGA
CCCCAGGTCTCTGGTAAACACTGAAAGCCTACTACTGGCCTGGTGCCCATCAATCATTGATCCTTGAGGCTG
TGCCCCCTGGGCACCCACCTGGCAGGGCTACCACCATGCACTGAGCTCCCTGTGGCTCTGCTGCCAGC
GCTTCCCTCATCTAGGGCTGTCTCTGGGTGCAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGG
GAGAAGATCCCTGTGAGGCTGTAGGGAGCAGGAGGGCCACAGAATCCAGATTGAGAGCTGGCTAGAC
CAAAGTGTGAAGACTTCAAAACCCGGATTGTCCTACTACAGGGACCCAACAAGCCCTACAAGAAGGTGCT
CAGGACTCGGTACATCCAGACAGAGCTGGCTCCCGTGAGGGTTGCTGGCTGTGACCTCCCGAGCTA
CACTGTCCACTTGGCGTGGCTGTGAAACCGTACGGTGGCCCATCACTCCCTCGTTACTCTACTCACTGG
CAGGGGGGGGGCGCTCCAGGGATGCAAGGTGGTGTCTCATGGGATGAGGGGGCGCTGGCTATGTC
AGAGACCCCTGCGCACCTTCACACACATTGGGGCGACTACGACTGGTCTTCATCATGCAAGGATGACACAT
ATGTGCAAGGCCCCCGCCTGGCAGCCCTGCTGGCACCTCAGCATCAACCAAGACCTGTACTTAGGCGGGCA
GAGGAGTTCAATTGGCGCAGGGAGCAGGCCGGTACTGTCTAGGGGCTTGGTACCTGGTACGGAGT
CCTGCTTCGTCTGGCCACATCTGGATGGCTGCCAGGAGACATTCTCAGTGCCTCTGACGAGTGGCTT
GACGCTGCCATTGACTCTGGCGCTGCTCACAGCACAGGGCAGCAGTATGCTCATTTGAA
CTGGCCAAAAAATAGGGACCTGAGAAGGAAGGGAGCTGGCTTCCTGAGTGCCTCGCCGTGACCCCTGCTC
CGAAGGTACCTCATGTACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGGGCTTACAGTAAATAG
AACAACTGCAGGCTCAGATCCGAACCTGACCGTGTGACCCCCGAAGGGAGGGCAGGGCTGAGCTGGCCGTT
GGGCTCCCTGCTCCTTCACACACACTCTCGCTTGGAGGTGCTGGCTGGACTACTTCACAGAGCAGCAC
CTTCTCCTGTGCAAGATGGGCTCCAAAGTGCCACTACAGGGGCTAGCAGGGCGACGTGGTGTGCTGG
AGACTGCCCTGGAGCAGCTCAATCGGCCTATCAGCCCCGCTGCGCTCCAGAAGCAGCAGTGCCTAACGGC
TATCGCGCTTCGACCCAGCACGGGATGGAGTACACCTGGACCTGCTGTTGAATGTGACACAGCGTGG
GCACCGGGGGCCCTGGCTCGCAGGGTCAAGCTGCTGCCACTGAGCCGGGTGAAATCTACCTATGCCCT
ATGTCACTGAGGCCACCCGAGTGCAGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGAGCCCCGGCTTTC
CTCGAGGGCTTTCAGCCAATGTCCTGGAGGCCACAGAGAACATGCAATTGCTCACCCCTGTTGGTCTACGGGCC
ACGAGAAGGTGGCGTGGAGCTCCAGAGCACCTTCTGGGGTGAAGGCTGAGCAGGGAGTTAGAGCAGGGT
ACCCCTGGGAGCAGGGCTGGCTGGCTCGCTGTGGAGCAGAGGGCCCTTCCCAGGTGCGACTCATGGACGTGGT
TCAAGAAGCACCCTGTGGACACTCTTCTTCTTACCAACCGTGTGGACAAGGCCCTGGCCGAAGTCTCAA
CCGCTGTCGCAATGCAATGCCATCTCTGGCTGGCAGGCCCTTCCAGTCCATTCCAGGAGTTCAATCCTGCC
TGTCAACACAGAGATCACCCCCAGGGCCCCGGGCTGGCCCTGACCCCCCTCCCTGGTGTGACCC
TCCCAGGGGGCTCTATAGGGGGAGATTGACGGCAGGCTTCTGCGAGGGCTGCTTACAACGCTGACTA
CCTGGCGGCCAGGCCGGCTGGCAGGTGAACCTGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGG
TGATGGATGTTTCTCCGGTTCTCAGGGCTCCACCTCTTCCGGCTAGAGCCAGGGCTGGTGCAGAAGTTC
TCCCTGGAGACTGCAGCCACGGCTCAGTGAAGAACTCTACCAACCGCTGCCGCTCAGCAACCTGGAGGGCT
AGGGGGCCGTGCCAGCTGGCTATGGCTCTTTGAGCAGGAGCAGGCCAATAGCACTTAGCCGCTGGGG
CCTAACCTCATTACCTTCTTGTCTGCCCTAGCCCCAGGAAGGGCAAGGAAGATGGTGGACAGATAGAGAA
TTGTTGCTGTATTTAAATATGAAAATGTTATTAAACATGTCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPPYRDPNPKPYKKVLTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSQHDERPAWLMSETLRHLHTFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDS LGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEI EQLQAQIRNLTVLTPEGAEAGLSWPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMEYTLDLLECVTQRGHRRALARRVSSLRPLSRVEILPMPYVTEATRVQLVLPLL
VAEAAAAPAFLEAFAANVLEPREHALLTL LVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFPALSPQRSPPGPPGAGPDPPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEAELEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRQLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372,
385-389, 399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCGTGC CGC GGCTGC GCTT CCT GTCCCCAAGCC
GTTCTAGACGCCGGAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTTGAAAATTCA
GAGGATGAGCGATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTGGACCAACACTGTGACAAAGCAG
AGTTCTCAGTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTGATAAGTATAGAGACCAATACAAC TG
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCT
CAATATCCCAGAAAAGTGCCTGAAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTAGATATGGCTGTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGTATACCGCTTAGGGCATTGGCATATTTCAAT
GATGCATTGGTTTCTTACCTCCAAATGGTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG
TGAATATGATTTGTATAGGACGTGTGTCATTATTTGTTAGTAGTAACATACATATCCAA
TACAGCTGTATGTTCTTTCTTTCTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGTAATG
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTTGCAAATAAAACTATTAATAAAATTATAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTTGCTGATTGGTT
AAAAAATTAAACAGGTCTTAGCGTTCAAGATATGCAAATGATATCTCTAGTIGTAATT
TGTGATTAAGTAAAACCTTAGCTGTGTTCCCTTACTTCTAATAACTGATTTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAGTGTAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNMDWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDQQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372,
385-389, 399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCYNYGSGVKNCCPLNWEYFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDATMRDSS
NPRQNWNDVTCLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCGCTGCCGTGGCCCCCTCAGCAACCCTGACATGGCGCTGAGGCGGCCACCGCGA
CTCCGGCTCTGCCTCGCTGCCTGACTTCTTCCTGCTGCTGCTTTCAGGGCTGCCTGATAGGGCTGTAAA
TCTCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTGCATCATACGGATT
CGCAGACAAGTGACCCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAAC
AAAATTAGGGAGACTTGGGGGTCGTGAGAAATACTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACG
GAGAGACTCAGCCCTTATCGCTGTGAGGTGCTGAAATGACCGCAAGGAATTGATGAGATTGTGATCG
AGTTAACCTGTGCAAGTGAAGCCAGTGACCCCTGCTGTAGAGTGCGAAGGCTGTACAGTAGGCAAGATGGCA
ACACTGCACTGCCAGGAGAGTGAGGGCCACCCCGGCCACTACAGCTGTATCGCAATGATGTACCACTGCC
CACGGATTCCAGAGCCAATCCCAGATTGCAATTCTCTTCACTTAAACTCTGAAACAGGCACTTGGTGT
TCACTGCTGTTACAAGGACACTCTGGCAGTACTACTGCATTGCTTCAATGACGCAGGCTCAGCCAGGTGT
GAGGAGCAGGAGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTCTGGGTGCTTGTGCTGT
ACTGGCCCTGATCACGTTGGCATTGCTGTGACAGACGCTGGCTACTTCATCAACAATAACAGGATGGAG
AAAGTTACAAGAACCCAGGGAAACCAGATGGAGTTAACATACATCCGCACTGACGAGGAGGGCGACTTCAGACAC
AAGTCATCGTTGTGATCTGAGACCCCGGTGTGAGAGCGCACAGAGCGCACGTGCACATACCTGCTA
GAAACTCTGTCAAGGCAGCGAGAGCTGATCGACTCGGACAGAGCTAGACACTCATCAGAAGCTTTGTTT
GCCAAAGTTGACCAACTCTTCTTAACAAAGGCCACATGAATAGAAGAATTTCCTCAAGATGACCCG
GTAAATATAACCAAGGAAGCGAAACTGGGTGCTCACTGAGTTGGGTCTTAATCTGTTCTGGCTGATT
CCCGCATGAGTATTAGGGTGATCTTAAAGAGTTGCTCACGTAACGCCCCGTGCTGGGCCCTGTGAAGGCAGCA
TGTTACCAACTGGTGTGAGCAGCACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACAGCAGCA
GCATCCCAGGGAAACCCAGAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAG
TTTCTCTTAAAGGCTCTGCTGATCGGTGTTGCACTGTCATTGTGAGAAGCTTTGGATCAGCATTTGTA
AAAACAACAAAATCAGGAAGGTAAATTGGGTGCTGGAAGAGGGATCTGCTGAGGAACCTGCTTGTCCAAC
AGGGTGTCAAGGATTAAGGAAAACCTCGTCTTAGGCTAAGTGTGAAATGGTACTGAAATATGCTTTATGG
GTCTTGTATTAAACATCTAAATTGCTAAGGATGTATTGATTATTGAAAAGAAAATT
CTATTTAAACTGTAAATATATTGTACATACAATGTTAAATAACCTATTAAAAAGTTCAACTTAAGGTAG
AAGTTCCAAGCTACTAGTGTAAATTGAAAATATCAATAATTAAAGGTATTACCAAGGAATCCTCTCATG
GAAGTTACTGTGATGTTCTTTCTCACACAAGTTTACAGCTTCAAGGAAACTCATACTGTCTACACA
TCAGACCATACTGGCTTAGGAAACCTTAAAATCCAGTTAACGCAATGTTGAAATCAGTTGCATCTCTCAA
AAGAAACCTCTCAGGTTAGCTTGAACTGCCTCTCCTGAGATGACTAGGACAGTCTGTACCCAGGGCACCC
AGAAGCCCTCAGATGTACATACACAGATGCCAGTCAGCTCTGGGTGCGCCAGGCGCCCCGCTCTAGCTCA
CTGTTGCCCTGCTGCTGCCAGGAGGCCCTGCCATCCTGGGCCCTGGCAGTGGCTGTGCTCCAGTGAGCTTTA
CTCACGTTGGCCCTGCTTACAGCACAGCTCAGGTGGCAGTGGCACACTGGTGTCTTCCATGTAGC
GTCCCAAGCTTGGCTCTGTAACAGACCTCTTTGGTTATGGATGGCTCACAAAATAGGGCCCAATTGCGAAATCAAGTCTG
TTTTTTTTTAAGTTGTTAAATTATTGTTAAGATTGCTTCAAGGCAAAGGCAATTGCGAAATCAAGTCTG
TCAAGTACAATAACATTTAAAAGAAAATGGATCCCAGCTGTTCTTCAAGGCAACAGAGAAAGCACCCAGACGC
CACAGGCTCTGCGATTCAAAACAAACCATGATGGAGTGGCGGCCAGTCCAGCCCTTTAAAGAACGTCAGGT
GGAGCAGCCAGGTGAAAGGCTGGCGGGAGGAAGTGAAACGCCCTGAATCAAAGCAGTTCTAATTGAC
TTAAATTTCATCCGCCAGACACTGCTCCCATTTGTGGGGGACATTAGCAACATCACTCAGAACGCTGT
GTTCTCAAGAGCAGGTGTTCTAGCCTCACATGCCCTGCCGTGCTGGACTCAGGACTGAAGTGTGAAAGCA
AGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCTGGAGAATGGCTCTCACTACTCACCTGCTTCA
CCAGTGTCTGGTTTTATACCTTGACAGCTTTTTAATTGCTACATGAGACTGTGTTGACTTTTTA
GTTATGTGAAACACTTGCGCAGGCCCTGGCAGAGGCAGGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTG
GTGTCTGCTGCATGGCATCTGGATGCTTAGCATGCAAGTCCCTCCATCATTGCCACCTGGTAGAGAGGGAT
GGCTCCCCACCCCTAGCGTTGGGATTACGCTCAGCCTCCTTGTGTTGCTAGTGATAGGGTAGCCTTA
TTGCCCTCTTCTTACCCCTAAACCTCTACACTAGTGCCTGGAAACCAGGTGAAAAAGTAGAGAGAA
GTGAAAGTAGAGTCTGGAAAGTAGCTGCCATATAACTGAGACTAGACGGAAAAGGAATAACTCGTGATTTAAGA
TATGAATGTGACTCAAGACTCGAGGCCATACGAGGCTGTGATTCTGCCTTGGATGGATGGTGTACACAG
ATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAACCTCATTATAAAAGCTTCAAAAAAAC
CA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLFLFRGCLIGAVNLKSSNRTPVVQEFESVELSCI ITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267